

GenCore version 5.1.3

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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 16:44:13 ; Search time 4314.97 Seconds
(without alignments)
11614.233 Million cell updates/sec

Title: US-09-826-581-3

Perfect score: 1722

Sequence: 1 cctggccctcagatcaaga.....gatgagagctcggtcgga 1722

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 15

Total number of hits satisfying chosen parameters: 69629

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: GenEmbl:

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vl.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1722	100.0	1722	6	AX281580	Sequence
C 2	1670	97.0	152129	2	AC027416	AX281580 Homo sapi
C 3	1479	85.9	206854	9	AC009974	AC009974 Homo sapi
4	168	9.8	1647	6	AX281582	Sequence
5	168	9.8	2109	6	AX099776	AX099776 Sequence
6	168	9.8	2115	6	AX099802	Sequence
7	168	9.8	2115	9	AF214519	AF214519 Homo sapi
8	168	9.8	2290	9	HS4249377	AJ249977 Homo sapi
9	57	3.3	106	11	G67375	G67375 A998 Human
C 10	39	2.3	227724	2	AF336381	AF336381 Mus muscu
11	38	2.2	1867	6	AX099774	AX099774 Sequence
12	38	2.2	1873	4	AF214520	AF214520 Sub scrof
13	38	2.2	1873	6	AX099800	Sequence
14	38	2.2	1873	6	AX398331	AX398331 Sequence
15	38	2.2	1873	6	AX398333	AX398333 Sequence
16	38	2.2	1873	6	AX398335	AX398335 Sequence
17	38	2.2	1873	6	AX398337	AX398337 Sequence
18	38	2.2	1873	6	AX398339	AX398339 Sequence
19	38	2.2	2022	6	AX099804	AX099804 Sequence
20	35	2.0	146577	2	AF214521	AF214521 Sus scrof
C 21	35	2.0	190183	2	AC128070	AC128070 Rattus no
C 22	35	2.0	192968	2	AC129703	AC129703 Rattus no
C 23	29	1.7	192968	2	AC127107	AC127107 Rattus no
C 24	29	1.7	192968	2	AC127107	AC127107 Rattus no
C 25	25	1.5	186248	2	AC026021	AC026021 Homo sapi
C 26	25	1.5	216497	9	HSDJ37C10	AL049569 Human DNA
27	24	1.4	1328	10	RNMFKGAM	X95578 R.norvegicu
C 28	24	1.4	1550	10	RNU42413	U42413 Rattus norv
C 29	24	1.4	5946	10	RATNESTIN	M34384 Rat nestin
C 30	24	1.4	184288	2	AC129422	AC129422 Rattus no
C 31	23	1.3	1194	9	AB046627	AB046627 Macaca fa
C 32	23	1.3	81704	9	AL512353	AL512353 Human DNA
C 33	23	1.3	82806	9	AC007111	AC007111 Homo sapi
C 34	23	1.3	192180	2	AC023331	AC023331 Homo sapi
C 35	23	1.3	196413	2	AC0097269	AC0097269 Pan trogl
C 36	23	1.3	198172	2	AC009065	AC009065 Homo sapi
37	23	1.3	239434	2	AC012171	AC012171 Homo sapi
38	22	1.3	74645	2	AC128292	AC128292 Rattus no
C 39	22	1.3	138312	9	AC026353	AC026353 Homo sapi
C 40	22	1.3	238325	2	AC105847	AC105847 Rattus no
C 41	21	1.2	2079	10	BC019836	BC019836 Mus muscu
42	21	1.2	41680	10	AF049091	AF049091 Mus muscu
43	21	1.2	58725	9	AC003988	AC003988 Human PAC
44	21	1.2	63680	2	AC101117	AC101117 Mus muscu
C 45	21	1.2	78215	2	AC105803	AC105803 Rattus no

ALIGNMENTS

RESULT 1
AX281580
LOCUS AX281580 1722 bp DNA linear PAT 03-NOV-2001
DEFINITION Sequence 3 from Patent WO0177305.
ACCESSION AX281580
VERSION AX281580.1 GI:16608831
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL

Andersson, L., Luthman, H. and Marklund, S.
Variants of the human amp-activated protein kinase gamma 3 subunit
Patent: WO 0177305-A 3 18-OCT-2001;

FEATURES	Arexis AB (SE)
source	Location/Qualifiers 1..1722 /organism="Homo sapiens" /db_xref="taxon:9606"
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Matches 1722; Conservative	0; Mismatches 0; Gaps 0;
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Db	1 CCTGGCCCTCAGATCAAGAAGCCCTTCTTCCTCTGTTGGCCAAAGGTGTGCGGGCAGC 60
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Db	61 CCCTCTATGGGACAGCAAGACAGAGCTTTCTGGGTGAGGAGAGCTTGGGAGGTGAAG 120
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AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavsky, L., Boukhgater, B., Brown, A., Burkett, G., Campolano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collimore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Hearford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Laroque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meidrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE
JOURNAL

Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jun 7, 2000 this sequence version replaced gi:7342115.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L7458

Center clone name: 504_G.11

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 135376 bases at least Q40

Consensus quality: 143264 bases at least Q30

Consensus quality: 146503 bases at least Q20

Insert size: 161000; agarose-fp

Quality coverage: 3.1 in Q20 bases; agarose-fp

Quality coverage: 3.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 1005: contig of 1005 bp in length
 * 1006 1105: gap of 100 bp
 * 1106 2402: contig of 1297 bp in length
 * 2403 2502: gap of 100 bp
 * 2503 3823: contig of 1321 bp in length
 * 3824 3923: gap of 100 bp
 * 3924 5020: contig of 1097 bp in length
 * 5021 5120: gap of 100 bp
 * 5121 6161: contig of 1041 bp in length
 * 6162 6261: gap of 100 bp
 * 6262 7547: contig of 1286 bp in length
 * 7548 7647: gap of 100 bp
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* 15044 15143: gap of 100 bp
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 * 17124 17223: gap of 100 bp
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 * 21929 22028: gap of 100 bp
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 * 24320 24419: gap of 100 bp
 * 24420 27059: contig of 2640 bp in length
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 * 73219 73318: gap of 100 bp
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 * 77116 77215: gap of 100 bp
 * 77216 85022: contig of 7807 bp in length
 * 85023 85122: gap of 100 bp
 * 85123 93314: contig of 8192 bp in length
 * 93315 93414: gap of 100 bp
 * 93415 101193: contig of 7779 bp in length
 * 101194 101293: gap of 100 bp
 * 101294 113090: contig of 11797 bp in length
 * 113091 113190: gap of 100 bp
 * 113191 123496: contig of 10306 bp in length
 * 123497 123596: gap of 100 bp
 * 123597 137837: contig of 14241 bp in length
 * 137838 137937: gap of 100 bp
 * 137938 152129: contig of 14192 bp in length.
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FEATURES

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 /clone_lib="RPC1-11 Human Male BAC"
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Db	36558	CCCTCTATGGACAGCAAGAGCAGAGCTTTGTGGGTGAGGAGGCTGGGAGGTGAAG	36499
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Qy	241	GGAGTCTGCATGCCAGCTGGGAGACCTCTGGGCTCAATTTCCCACTCTGTGGAGCCGT	300
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Qy	301	ATGACGAGTGACACTTTACCTCCGCTACTGCAATGGCCCTGTGCCATAGGTGCTAGGG	360
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Qy	361	AGCAATGGGGGAGCGAGAGAGAGCCCACTTCTCAGGCTTGGGGGCTGCCCC	420
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Db	36198	ACTGTCTCTGTCCACAGTCCCACTGTGTCTCAGCACAAAGACACTGGCAGGGTGGGA	36139
Qy	481	GGGGATCTGACCTCAACTGCTCTCCACCCAAAGGCCCGGGGTGACTCTCTCCCGCC	540
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Qy	1261	CACCTCATCAAGAACCGGATCCATCGCTGCTGTCTTGACCCGGTGTGAGGCAAGCT	1320
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Qy	1321	ACTCCACATCTCACACAAAGCGCTGTCAAGTTCTTCACATCTTTTGAAGCTGTGG	1380
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Db 35118 ACCTGGTCCCATCTTAACAGGGTTCCCTGCTGCGCGGCCCTCTTCTCTACCGCAC 35059
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RESULT 3
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LOCUS AC009974 206854 bp DNA linear PRI 09-JAN-2002
DEFINITION Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
ACCESSION AC009974
VERSION AC009974.9 GI:16799058
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 206854)
AUTHORS Harris,A. and Cotton,M.
TITLE The sequence of Homo sapiens BAC clone RP11-459119
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 6 (bases 1 to 206854)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 8, 2001 this sequence version replaced gi:13431203.
-----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
-----
Summary Statistics
Center project name: H_NH0459119
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```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPC1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Moon,P.Y., Zhao,B., Frengen,E., Tateo,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACes.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. An unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

FEATURES

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Db 165619 ACAGTCCCTCCCTCCAGTCCCACTAGCTCTGAACCTACCTCTTCACTAGCGCGGACA 165560

QY 1141 CAGACAAGGAGCCTTGGTGCCCTGCTCTCTTTTATAGGGGCTCGGATGGAGGTGTCT 1200

Db 165559 CAGACAAGGAGCCTTGGTGCCCTGCTCTCTTTTATAGGGGCTCGGATGGAGGTGTCT 165500

QY 1201 CTCCTAGCTGCCCGAGGCTCATGTCTCCATCTCTGCAGCCTGTTTGAAGCTGTCTA 1260

Db 165499 CTCCTAGCTGCCCGAGGCTCACTGTCTCCATCTCTGCAGCCTGTTTGAAGCTGTCTA 165440

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Db 165439 CACCTCTCATCAAGAACCGATCCATCGCTGCTCTTTCAGCCGGTGTGAGGCAAGT 165380

QY 1321 ACTCCACATCTTCACACAAACGCTGCTCAAGTTCCTGACATCTTTTGAAGCTGTGG 1380

Db 165379 ACTCCACATCTTCACACAAACGCTGCTCAAGTTCCTGACATCTTTTGAAGCTGTGG 165320

QY 1391 CCCAGTGGGAGGAGGCGGAGACCTGGGAGGTGATCAGAGGCTGAGAGTCTTCAG 1440

Db 165319 CCCAGTGGGAGGAGGCGGAGACCTGGGAGGTGATCAGAGGCTGAGAGTCTTCAG 165260

QY 1441 CCCTAGCAGTCTGTGGGAGAGCTGGGAGCCTCTTGAAGCTGTGGATCCCTGATCTCC 1500

Db 165259 CCCTAGCAGTCTGTGGGAGAGCTGGGAGCCTCTTGAAGCTGTGGATCCCTGATCTCC 165200

QY 1501 ACCTGGTCCCATCTAACCAGGTTCTCTGCTGCCCGGCCCTCTCTCTACCGCAC 1560

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QY 1681 CGAATGTGTTACCCACCCAGGATGAGAGCTCGGCTGG 1721

Db 165019 CGAATGTGTTACCCACCCAGGATGAGAGCTCGGCTGG 164979

RESULT 4
AX281582
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AX281582
Sequence 5 from Patent WO0177305.
AX281582
AX281582.1 GI:16608833
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Andersson, L., Luthman, H. and Marklund, S.
Variants of the human amp-activated protein kinase gamma 3 subunit
Patent: WO 0177305-A 5 18-OCT-2001;
Arexis AB (SE)
Location/Qualifiers
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BASE COUNT 346 a 502 c 462 g 337 t

ORIGIN

Query Match 9.8%; Score 168; DB 6; Length 1647;
Best Local Similarity 100.0%; Pred. No. 2.6e-78;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1523 GGTTCCTGCTGCCCCGCCCTCTCTCTACCGCACTATCCAAGATTTGGGCATCGGC 1582

Db 1022 GGTTCCTGCTGCCCCGCCCTCTCTCTACCGCACTATCCAAGATTTGGGCATCGGC 1081

QY 1583 ACATTCGAGACTTGGCTGTGGTGTGGAGACAGACACCCATCTCTGACTGGACATC 1642

Db 1082 ACATTCGAGACTTGGCTGTGGTGTGGAGACAGACACCCATCTCTGACTGGACATC 1141

QY 1643 TTTGTGAGACCGGCTGTCTGCACTGCCCTGCTGCTCAACGAATGTGGT 1690

Db 1142 TTTGTGAGACCGGCTGTCTGCACTGCCCTGCTGCTCAACGAATGTGGT 1189

RESULT 5
AX099776
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AX099776
Sequence 3 from Patent WO0120003.
AX099776
AX099776.1 GI:13538810
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2109)
Rogel-Gaillard, C., Looft, C., Kalm, E., Milan, D., Robic, A.,
Chardon, P.
Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
Location/Qualifiers
1. .2109
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BASE COUNT 458 a 621 c 560 g 470 t

ORIGIN

Query Match 9.8%; Score 168; DB 6; Length 2109;
Best Local Similarity 100.0%; Pred. No. 2.5e-78;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1523 GGTTCCTGCTGCCCCGCCCTCTCTCTACCGCACTATCCAAGATTTGGGCATCGGC 1582

Db 922 GGTTCCTGCTGCCCCGCCCTCTCTCTACCGCACTATCCAAGATTTGGGCATCGGC 981


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DEFINITION Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit
              (AMPK gamma 3 gene).
ACCESSION   AJ249977
VERSION     AJ249977.1 GI:6688200
KEYWORDS    AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2290)
AUTHORS    Cheung,P.C., Salt,I.P., Davies,S.P., Hardie,D.G. and Carling,D.
TITLE       Characterization of AMP-activated protein kinase gamma-subunit
            isoforms and their role in AMP binding
JOURNAL     Biochem. J. 346 Pt 3, 659-669 (2000)
MEDLINE     20164049
PUBMED      10698692
REFERENCE   2 (bases 1 to 2290)
AUTHORS    Carling,D.
TITLE       Direct Submission
JOURNAL     Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC
            Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,
            London, W12 0NN, UNITED KINGDOM
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            Location/Qualifiers
                1..2290
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                Best Local Similarity 100.0%; Pred. No. 2.4e-78;
                Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1523 GGTTCCTGTGTCGCCGCCCTCTCTCTACCGCACTATCCAGATTTTGGGCATCGGC 1582
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Db 1024 GGTTCCTGTGTCGCCGCCCTCTCTCTACCGCACTATCCAGATTTTGGGCATCGGC 1083

Qy 1583 ACATTCGAGACTTGGCTGCTGTGAGACAGACACCCATCTCTGACTGCACTGGACATC 1642
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Qy 1643 TTTGTGACCCGCCGTGTGCTGTGCACTGCTGTGTGTCACGAATGTGGT 1690
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LOCUS      A898 Human Homo sapiens STS genomic, sequence tagged site.
DEFINITION A898 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION   G67375
VERSION     G67375.1 GI:11841655
KEYWORDS    STS.

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SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 106)
AUTHORS    Robic,A., Jeon,J.-T., Rey,V., Amarger,V., Chardon,P., Looft,C.,
            Andersson,L., Gellin,J. and Milan,D.
TITLE       Construction of a high-resolution RH map of human 2q35 region on
            TNG panel and comparison with physical map of porcine homologous
            region 15q25
JOURNAL     Unpublished (2001)
COMMENT     Contact: Annie ROBIC, Denis MILAN
            Genetique Cellulaire
            Institut National de Recherche agronomique (INRA)
            BP27, 31326 Castanet Tolosan, France
            Tel: (33) 5 61 28 51 21
            Fax: (33) 5 61 28 53 08
            Email: arobic@coulouse.inra.fr
            Primer A: TGGGATCGGCACATTCC
            Primer B: GACCACAGGACGTGCAGCA
            PCR Profile:
            Initial incubation: 94 degrees C for 4 min
            Denaturation: 94 degrees C for 30 seconds
            Annealing: 55 degrees C for 30 seconds
            Polymerization: 72 degrees C for 30 seconds
            PCR cycles: 33
            Thermal cycler: Perkin Elmer 9600
            Protocol:
            Template: 25 ng
            Primer: each 0.5 uM
            dNTPs: each 200 uM
            Taq Polymerase: 0.1 units/reaction
            Total Vol: 15 ul
            Buffer:
            MgCl2: 2 mM
            KCl: 50 mM
            Tris-HCl: 20 mM
            pH: 8.4
            Primers were defined on sequence AAL78898 (cDNA). No intron.
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                Best Local Similarity 100.0%; Pred. No. 2e-18;
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Qy 1622 ATCTGACTGCACTGACATCTTTGTGGACCGCGTGTGTCTGCACTGCTGTGGTC 1678
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Db 50 ATCTGACTGCACTGACATCTTTGTGGACCGCGTGTGTCTGCACTGCTGTGGTC 106

RESULT 10
AF336381/c
LOCUS      AF336381
DEFINITION Mus musculus chromosome 1 clone PAC510; PAC457, *** SEQUENCING IN
            PROGRESS ***, 3 unordered pieces.
ACCESSION   AF336381
VERSION     AF336381.1 GI:13507298
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Mus musculus.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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REFERENCE
AUTHORS      Rump,A., Hayes,C., Brown,S.D.M. and Rosenthal,A.
TITLE        Mouse chromosome 1 genomic sequence
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 227724)
AUTHORS      Rump,A.
TITLE        Direct Submission
JOURNAL      Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular
              Biotechnology, Beutenbergstr. 11, Jena 07745, Germany
COMMENT      * NOTE: This is a 'working draft' sequence. It currently
              * consists of 3 contigs. The true order of the pieces
              * is not known and their order in this sequence record is
              * arbitrary. Gaps between the contigs are represented as
              * runs of N, but the exact sizes of the gaps are unknown.
              * This record will be updated with the finished sequence
              * as soon as it is available and the accession number will
              * be preserved.
              * 1 17869: contig of 17869 bp in length
              * 17870 17969: gap of unknown length
              * 17970 32746: contig of 14777 bp in length
              * 32747 32846: gap of unknown length
              * 32847 227724: contig of 194878 bp in length.
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Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 TGGACAGCAGAGAGCAGAGCTTTGTGGTGAGGAGAG 106
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Db 6807 TGGACAGCAGAGAGCAGAGCTTTGTGGTGAGGAGAG 6769
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RESULT 11
AX099774
LOCUS      AX099774
DEFINITION Sequence 1 from Patent WO0120003.
ACCESSION  AX099774
VERSION     AX099774.1 GI:13538808
KEYWORDS   '
SOURCE      pig.
ORGANISM    Sus scrofa
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1 (bases 1 to 1867)
AUTHORS     Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
             Rogel-Gaillard,C., Looft,C., Kalm,E., Gellin,J., le Roy,P. and
             Chardon,P.
TITLE       Variants of the gamma chain of ampk, dna sequences encoding the
             same, and uses thereof
JOURNAL     Patent: WO 0120003-A 1 22-MAR-2001;
             INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
             Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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Query Match      2.2%; Score 38; DB 6: Length 1867;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1562 ATCCACAGATTGGGCATCGGCACATTCGAGACTTGGC 1599
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Db 961 ATCCACAGATTGGGCATCGGCACATTCGAGACTTGGC 998
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RESULT 12
AF214520
LOCUS      AF214520
DEFINITION Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
             mRNA, complete cds.
ACCESSION  AF214520
VERSION     AF214520.1 GI:8215683
KEYWORDS   '
SOURCE      Sus scrofa.
ORGANISM    Sus scrofa
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1 (bases 1 to 1873)
AUTHORS     Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
             Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
             Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
             and Andersson,L.
TITLE       A mutation in PRKAG3 associated with excess glycogen content in pig
             skeletal muscle
JOURNAL     Science 288 (5469), 1248-1251 (2000)
MEDLINE     20280150
PUBMED      10818001
REFERENCE   2 (bases 1 to 1873)
AUTHORS     Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
             Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
             Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
             Direct Submission
TITLE       Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
             University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
             Sweden
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             HFQWQHTCYDAMATSSKLVIKFAFFALVANGVRAAPLWDSKQSFVGLMTI
             TDFILVLYRSPVLQVIEIEHKIETWREIYVQCPRPLVSISPNDLSFAYALI
             KNRIHRLPVLDPVSGAVLHILTHKRLKLFHIFGTLPRPSFLYRTIQDLGIGTRDL
             AVVLETAIPLTALDIFVDRVSALPVVNETGVVGLYSRFDVIHLAAQOTYHLDNNTV
             CEALRQRTLCLEGLVSCQPHETLGEVIDRIVREQVHRLVLVDETOHLGVSVSLDILQ
             ALVSPAGIDALGA"
BASE COUNT  382 a 580 c 535 g 376 t
ORIGIN
Query Match      2.2%; Score 38; DB 4: Length 1873;

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Qy 1562 ATCCAAGATTGGGCATCGGCACATTCGAGACTTGGC 1599
|||||
Db 967 ATCCAAGATTGGGCATCGGCACATTCGAGACTTGGC 1004
|||||

Search completed: January 7, 2003, 20:11:10
Job time : 4937.97 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 17:17:03 ; Search time 479.092 Seconds
(without alignments)
1486.844 Million cell updates/sec

Title: US-09-826-581-5
Perfect score: 1647
Sequence: 1 ttggtctggggctggccaca.....acaccagctcttagtcttc 1647

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 381593 seqs, 216252194 residues

Word size : 15

Total number of hits satisfying chosen parameters: 1247

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1647	100.0	1647	US-09-826-581-5	Sequence 5, Appli
2	406	24.7	989	US-09-826-581-2	Sequence 2, Appli
3	278	16.9	1014	US-09-826-581-4	Sequence 4, Appli
4	168	10.2	1722	US-09-826-581-3	Sequence 3, Appli
5	85	5.2	378	US-09-864-761-1373	Sequence 373, Ap
6	54	3.3	92	US-09-864-761-20146	Sequence 20146, A
7	52	3.2	821	US-09-826-581-1	Sequence 1, Appli
8	20	1.2	333	US-09-974-300-1402	Sequence 1402, Ap
9	19	1.2	1411	US-09-935-720-2	Sequence 2, Appli
10	19	1.2	7771	US-09-832-292-38	Sequence 38, Appli
11	18	1.1	153	US-09-864-761-22801	Sequence 22801, A
12	18	1.1	325	US-09-960-352-2438	Sequence 2438, Ap
13	18	1.1	394	US-09-867-701-968	Sequence 968, App
14	18	1.1	459	US-09-864-761-6044	Sequence 6044, Ap
15	18	1.1	487	US-09-962-436-230	Sequence 230, App
16	18	1.1	487	US-09-880-107-1075	Sequence 1075, Ap
17	18	1.1	3364	US-09-925-300-665	Sequence 665, App
18	18	1.1	6746	US-09-919-497-18	Sequence 18, Appli
19	18	1.1	6746	US-09-967-768A-303	Sequence 303, App

ALIGNMENTS

RESULT 1

US-09-826-581-5

; Sequence 5, Application US/09826581

; Patent No. US20020142310A1

; GENERAL INFORMATION:

; APPLICANT: Andersson, Leif

; APPLICANT: Luchman, L. Holger

; APPLICANT: Marklund, Stefan

; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT

; FILE REFERENCE: 11145-007001

; CURRENT APPLICATION NUMBER: US/09/826.581

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: US 60/195,665

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 1647

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (20)...(1486)

US-09-826-581-5

Query Match	100.0%	Score 1647;	DB 10;	Length 1647;
Best local Similarity	100.0%;	Pred. No. 0;		
Matches 1647;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TTGTCCTGGGGCTGGCCACATGGAGCCCGGCTGGAGCAGCACTGGCGCAGGACCCCTTC	60	
Db	1	TTGTCCTGGGGCTGGCCACATGGAGCCCGGCTGGAGCAGCACTGGCGCAGGACCCCTTC	60	
Qy	61	CTGAGCAGCCTTGGGGGTTCTGAGCATCAAGAGATGAGCTTCTTAGAGCAAGAAACAG	120	
Db	61	CTGAGCAGCCTTGGGGGTTCTGAGCATCAAGAGATGAGCTTCTTAGAGCAAGAAACAG	120	
Qy	121	CAGTCATGGCCATCACCAGCTGTGACCAGCCTGAGAAAGAAATCCGTGGGAAACGGAG	180	
Db	121	CAGTCATGGCCATCACCAGCTGTGACCAGCCTGAGAAAGAAATCCGTGGGAAACGGAG	180	
Qy	181	GGCCAAAGCCTTGAGATGGCAAGGAGGAGTGGTGGGAGGAGGAGGCCACCGAGTCA	240	

[illegible]

Db	1261	CATGAGTGTGGGGAAGCCCTGAGGCAGAGGACACTATGTTCTGGAGGGAGTCTTTCCTG	1320
QY	1321	CCAGCCCCACAGAGCTTTGGGGAAGTGATCGACAGGATGTTCTCGGAGCAGGTACACAG	1380
Db	1321	CCAGCCCCACAGAGCTTTGGGGAAGTGATCGACAGGATGTTCTCGGAGCAGGTACACAG	1380
QY	1381	GCTGTTGCTAGTGACGAGACCCAGCATCTCTTTGGCGTGTCTCCCTCTCCGACATCCT	1440
Db	1381	GCTGTTGCTAGTGACGAGACCCAGCATCTCTTTGGCGTGTCTCCCTCTCCGACATCCT	1440
QY	1441	TCAGGCACTGGTGTCTAGCCCTCTCGCATCGATGCCCTCGGGGCTTGAGAAAGATCTGAG	1500
Db	1441	TCAGGCACTGGTGTCTAGCCCTCTCGCATCGATGCCCTCGGGGCTTGAGAAAGATCTGAG	1500
QY	1501	TCCTCAATCCCAAGCCACCTGACACCTCGAAGCCAAATGMAAGGAACTGGAGAATCAGC	1560
Db	1501	TCCTCAATCCCAAGCCACCTGACACCTCGAAGCCAAATGMAAGGAACTGGAGAATCAGC	1560
QY	1561	CTTCATCTTCCCAACCCCAATTTGCTGGTATGATTCAGGTAGGCTCTGCCCTG	1620
Db	1561	CTTCATCTTCCCAACCCCAATTTGCTGGTATGATTCAGGTAGGCTCTGCCCTG	1620
QY	1621	GGCCATGACACCCAGCTCTTAGTCTTC	1647
Db	1621	GGCCATGACACCCAGCTCTTAGTCTTC	1647
RESULT 2			
US-09-826-581-2			
; Sequence 2, Application US/09826581			
; Patent No. US20020142310A1			
; GENERAL INFORMATION:			
; APPLICANT: Andersson, Leif			
; APPLICANT: Luthman, L. Holger			
; APPLICANT: Marklund, Stefan			
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE G			
; FILE REFERENCE: 11145-007001			
; CURRENT APPLICATION NUMBER: US/09/826,581			
; CURRENT FILING DATE: 2001-04-05			
; PRIOR APPLICATION NUMBER: US/60/195,665			
; PRIOR FILING DATE: 2000-04-07			
; NUMBER OF SEQ ID NOS: 14			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 2			
; LENGTH: 989			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-826-581-2			
Query Match 24.7%; Score 406; DB 10; Length 989;			
Best Local Similarity 100.0%; Pred. No. 4.2e-191;			
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps			
QY	247	AGGTCCCGGTCCAGGCAGCTGTGATCCACCGGCTGGAGGCCACATTCCCCCAAGAC	306
Db	540	AGGTCCCGGTCCAGGCAGCTGTGATCCACCGGCTGGAGGCCACATTCCCCCAAGAC	599
QY	307	CACACCTTTGGCTCAAGCTGATCTCCCGGGTGGGCACCTCCACCAACGGGTGGGACTG	366
Db	600	CACACCTTTGGCTCAAGCTGATCTCCCGGGTGGGCACCTCCACCAACGGGTGGGACTG	659
QY	367	CTTCCCTCTGACTGTACAGCTTCAGCTGCAGGCTCCAGCACAGATGATGTGAGCTGGC	426
Db	660	CTTCCCTCTGACTGTACAGCTTCAGCTGCAGGCTCCAGCACAGATGATGTGAGCTGGC	719
QY	427	CACGAGATTCCAGCCACAGAGGCTTGGAGTGTGAGCTAGAGGCTTGCGGAAGAGAG	486
Db	720	CACGAGATTCCAGCCACAGAGGCTTGGAGTGTGAGCTAGAGGCTTGCGGAAGAGAG	779
QY	487	GCCTGCCCTGTGCTGTCTCCCGCAGGCCCAATTTTCCCAAGCTGGGTGGGATCACCACCT	546
Db	780	GCCTGCCCTGTGCTGTCTCCCGCAGGCCCAATTTTCCCAAGCTGGGTGGGATCACCACCT	839

[illegible]

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RESULT 3
US-09-826-581-4
; Sequence 4, Application US/09826581
; Patent No. US2002014210A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-4

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Query Match	16.9%	Score 278;	DB 10;	Length 1014;
Best Local Similarity	100.0%;	Pred. No. 9e-128;		
Matches 278;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1370	CAGGTACACAGGCTGGTGCTAGTGCAGAGACCCAGACATCTCTTGGGCGTGGTCTCCCTC	1429		
Db	737 CAGGTACACAGGCTGGTGCTAGTGCAGAGACCCAGACATCTCTTGGGCGTGGTCTCCCTC	796		
QY 1430	TCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATCGATGCCCTCGGGGCGCTGA	1489		
Db	797 TCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATCGATGCCCTCGGGGCGCTGA	856		
QY 1490	GAAGATCTGATGCTCTCAATCCCAAGCCACCTGCGACACCTCGGAAGCCAATGAAGGGAACGT	1549		
Db	857 GAAGATCTGATGCTCTCAATCCCAAGCCACCTGCGACACCTCGGAAGCCAATGAAGGGAACGT	916		
QY 1550	GAGAATCTCAGCCTTCATCTTCCCCACCCCATTTGCTGGTTCAGCTATGATCAGGTAG	1609		
Db	917 GAGACTCAGCCTTCATCTTCCCCACCCCATTTGCTGGTTCAGCTATGATCAGGTAG	976		
QY 1610	GCTCTGCCCTGGGCCATGACACCAAGCCTCTTAGTCTTTC	1647		
Db	977 GCTCTGCCCTGGGCCATGACACCAAGCCTCTTAGTCTTTC	1014		

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RESULT 4
US-09-826-581-3
; Sequence 3, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

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; LENGTH: 1722
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-3

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Query Match 10.2%; Score 168; DB 10; Length 1722;
Best Local Similarity 100.0%; Pred. No. 2.4e-73;
Matches 168; Conservative 0; Mismatches 0; Indels 0

RESULT 5
US-09-864-761-3373/c
; Sequence 3373, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US 09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263 .6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20146
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009974.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
; OTHER INFORMATION: NT HIT: g11430152, EVALUE 2.00e-22
; OTHER INFORMATION: EST HUMAN HIT: BE327467.1, EVALUE 3.00e-06
; OTHER INFORMATION: SWISSPROT HIT: P54619, EVALUE 3.00e-03
US-09-864-761-20146

Query Match 3.3%; Score 54; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.9e-17;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 651 AGATCAAGAGGCCCTCTTTGGCTCTGGTGCCCAACGGTGTGGCGGAGCCCTC 704
Db 54 AGATCAAGAGGCCCTCTTTGGCTCTGGTGCCCAACGGTGTGGCGGAGCCCTC 1

RESULT 7
US-09-826-581-1
; Sequence 1, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUB
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-1

Query Match 3.2%; Score 52; DB 10; Length 821;
Best Local Similarity 100.0%; Pred. No. 5.8e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGTCTGGGGCTGGCCACATGAGCCCCGGGCTGGAGCAGCACTCGCAGG 52
Db 313 TTGGTCTGGGGCTGGCCACATGAGCCCCGGGCTGGAGCAGCACTCGCAGG 364

RESULT 8

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US-09-974-300-1402
; Sequence 1402, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods for Monitoring Multiple Gene
; FILE REFERENCE: 10085 500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1402
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-1402

Query Match          1.2%; Score 20; DB 10; Length 333;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 GACCAGCGCTCAGAAAGAA 164
Db 265 GACCAGCGCTCAGAAAGAA 284

RESULT 9
US-09-935-720-2
; Sequence 2, Application US/09935720
; Patent No. US20020156260A1
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHIO
; KAISHO, NISHINOMIYA
; TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
; PRE-B CELL GROWTH-SUPPORTING ABILITY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER& NEUSTADT,
; P. C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,720
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/09/517,739
; FILING DATE: 23-DEC-1997
; APPLICATION NUMBER: US/08/997,252
; FILING DATE: 23-DEC-1997
; APPLICATION NUMBER: US 08/537,942
; FILING DATE: 21-NOV-1995
; APPLICATION NUMBER: PCT/JP94/00819
; FILING DATE: 20-MAY-1994
; APPLICATION NUMBER: JP 5-141178
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
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; REFERENCE/DOCKET NUMBER: 4767-0005-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..84
; IDENTIFICATION METHOD: /note= "IDENTIFICATION METHOD: E"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-935-720-2

Query Match          1.2%; Score 19; DB 9; Length 1411;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1112 ACAGCACCCATCCTGACTG 1130
Db 948 ACAGCACCCATCCTGACTG 966

RESULT 10
US-09-832-292-38/c
; Sequence 38, Application US/09832292
; Patent No. US20020177205A1
; GENERAL INFORMATION:
; APPLICANT: Ryazanov, Alexey
; TITLE OF INVENTION: MAMMALIAN ALPHA-KINASE PROTEINS, NUCLEIC ACIDS AND
; FILE REFERENCE: 601-1-098CIP
; CURRENT APPLICATION NUMBER: US/09/832,292
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 09/632,131
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 7771
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-832-292-38

Query Match          1.2%; Score 19; DB 9; Length 7771;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 AGGCAGAAAGTCGGTGAGG 221
Db 4855 AGGCAGAAAGTCGGTGAGG 4837

RESULT 11
US-09-864-761-22801
; Sequence 22801, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
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;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Amonax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 22801
;; LENGTH: 153
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC003104.1
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
;; OTHER INFORMATION: EST_HUMAN HIT: AW749933.1, EVALUATE 2.00e-71
;; OTHER INFORMATION: NT HIT: g11426182, EVALUATE 1.00e-71
US-09-864-761-22801

Query Match 1.1%; Score 18; DB 10; Length 153;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 737 ATGCTGACCATCACTGAC 754
Db 96 ATGCTGACCATCACTGAC 113
|||||

RESULT 12
US-09-960-352-2438
;; Sequence 2438, Application US/09960352
;; Patent No. US20020137139A1
;; GENERAL INFORMATION:
;; APPLICANT: Warren, Wesley C.
;; APPLICANT: Ieo, Nengbing
;; APPLICANT: Byatt, John C.
;; APPLICANT: Mathialagan, Nagappan
;; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

;; FILE REFERENCE: 16511.006/37-21(10298)C
;; CURRENT APPLICATION NUMBER: US/09/960,352
;; CURRENT FILING DATE: 2001-09-24
;; NUMBER OF SEQ ID NOS: 15112
;; SEQ ID NO 2438
;; LENGTH: 325
;; TYPE: DNA
;; ORGANISM: Bos taurus
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (240)
;; OTHER INFORMATION: unsure at all n locations
;; OTHER INFORMATION: Clone ID: 11-LIB3058-018-Q1-K1-C3
US-09-960-352-2438

Query Match 1.1%; Score 18; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 214 GGTGGAGGAGGGGAGCC 231
Db 18 GGTGGAGGAGGGGAGCC 35
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RESULT 13
US-09-867-701-968/c
;; Sequence 968, Application US/09867701
;; Patent No. US20020132237A1
;; GENERAL INFORMATION:
;; APPLICANT: Aglate, Paul A.
;; APPLICANT: Jones, Robert
;; APPLICANT: Harlocker, Susan L.
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;; FILE REFERENCE: 210121.497
;; CURRENT APPLICATION NUMBER: US/09/867,701
;; CURRENT FILING DATE: 2001-05-29
;; NUMBER OF SEQ ID NOS: 10912
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 968
;; LENGTH: 394
;; TYPE: DNA
;; ORGANISM: Homo sapien
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)...(394)
;; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-968

Query Match 1.1%; Score 18; DB 10; Length 394;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1627 GACACCAGCCTCTTAGTC 1644
Db 38 GACACCAGCCTCTTAGTC 21
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RESULT 14
US-09-864-761-6044
;; Sequence 6044, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;; FILE REFERENCE: Aeonica-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312

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; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 6044
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC003104.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
US-09-864-761-6044

Query Match
Best Local Similarity 1.1%; Score 18; DB 10; Length 459;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 737 ATGCTGACCATCACTGAC 754
Db 125 ATGCTGACCATCACTGAC 142
|||||

RESULT 15
US-09-962-436-230
; Sequence 230, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE OF INVENTION: Secs
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
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; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 230
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-230

Query Match
Best Local Similarity 1.1%; Score 18; DB 10; Length 487;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 440 GCCACAGAGGCGCTGGGAG 457
Db 53 GCCACAGAGGCGCTGGGAG 70
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Job time : 492.092 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 20:16:02 ; Search time 62.0864 Seconds
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Title: US-09-826-581-5
Perfect score: 1647
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 15

Total number of hits satisfying chosen parameters: 737

Minimum DB seq length: 0

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- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq:*
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- 5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	19	1.2	1411	1	US-08-537-942A-2
2	19	1.2	1411	4	US-08-997-252A-2
3	19	1.2	1411	4	US-09-517-739-2
4	17	1.0	423	1	US-08-470-179-189
5	17	1.0	1419	2	US-08-194-981E-4
6	17	1.0	1545	2	US-08-660-963-9
7	17	1.0	1576	3	US-09-101-146-63
8	17	1.0	1591	2	US-08-194-981E-3
9	17	1.0	1703	3	US-08-646-273-18
10	17	1.0	1852	1	US-08-201-118-10
11	17	1.0	1852	2	US-08-238-821B-10
12	17	1.0	1852	5	PCT-US95-05744-10
13	17	1.0	1854	1	US-08-201-118-4
14	17	1.0	1854	2	US-08-238-821B-4
15	17	1.0	1854	5	PCT-US95-05744-4
16	17	1.0	2129	3	US-08-646-273-22
17	17	1.0	2314	3	US-08-646-273-29
18	17	1.0	2707	2	US-08-709-874A-9
19	17	1.0	2707	4	US-09-104-382-9
20	17	1.0	2889	1	US-08-289-112-1
21	17	1.0	2907	2	US-09-018-628-17
22	17	1.0	2907	3	US-09-273-378-17
23	17	1.0	2907	4	US-09-018-635-26
24	17	1.0	2907	4	US-09-467-642-3
25	17	1.0	3697	1	US-08-571-758-1
26	17	1.0	3697	1	US-08-909-984A-1
27	17	1.0	3697	1	US-08-909-983-1

28	17	1.0	4127	4	US-09-487-368A-10	Sequence 10, Appl
c 29	17	1.0	6453	1	US-08-306-691B-14	Sequence 14, Appl
c 30	17	1.0	6453	3	US-09-209-668-10	Sequence 10, Appl
c 31	17	1.0	6453	3	US-09-356-952-8	Sequence 8, Appl
c 32	17	1.0	9551	1	US-08-056-200-93	Sequence 93, Appl
c 33	17	1.0	9551	2	US-08-800-644-93	Sequence 60, Appl
34	17	1.0	15652	4	US-09-422-936-60	Sequence 93, Appl
35	17	1.0	28473	4	US-08-961-527-83	Sequence 83, Appl
36	17	1.0	65042	4	US-09-784-316-3	Sequence 3, Appl
37	17	1.0	84495	4	US-09-797-906-3	Sequence 3, Appl
38	17	1.0	111282	4	US-09-754-250-3	Sequence 3, Appl
c 39	17	1.0	4411529	4	US-09-103-840A-1	Sequence 1, Appl
40	16	1.0	21	3	US-08-784-551C-3	Sequence 3, Appl
41	16	1.0	36	1	US-07-936-421-15	Sequence 15, Appl
42	16	1.0	77	5	PCT-US95-10973A-19	Sequence 19, Appl
43	16	1.0	146	3	US-08-765-340-9	Sequence 9, Appl
44	16	1.0	239	1	US-08-248-474-47	Sequence 47, Appl
45	16	1.0	239	3	US-08-756-849-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-08-537-942A-2
; Sequence 2, Application US/08537942A
; Patent No. 5753464
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHIO
; APPLICANT: KAISHO, NISHINOMIYA
; TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
; TITLE OF INVENTION: PRE-B CELL GROWTH-SUPPORTING ABILITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,942A
; FILING DATE: 21-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00819
; FILING DATE: 20-MAY-1994
; PRIOR APPLICATION DATA: JP 5-141178
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4767-004-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..84

; OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"
US-08-537-942A-2

Query Match 1.2%; Score 19; DB 1; Length 1411;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1112 ACAGCACCCTCTGACTG 1130

DB 948 ACAGCACCCTCTGACTG 966

RESULT 2

US-08-997-252A-2
; Sequence 2, Application US/08997252A
; Patent No. 6232453
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHIO
; APPLICANT: KAISHO, NISHINOMIYA
; TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
; PRE-B CELL GROWTH-SUPPORTING ABILITY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,252A
; FILING DATE: 23-DEC-1997

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/537,942
; FILING DATE: 21-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00819
; FILING DATE: 20-MAY-1994

REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4767-0005-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:

NAME/KEY: sig_peptide
; LOCATION: 1..84
; OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"

US-08-997-252A-2

Query Match 1.2%; Score 19; DB 4; Length 1411;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1112 ACAGCACCCTCTGACTG 1130

DB 948 ACAGCACCCTCTGACTG 966

RESULT 3

US-09-517-739-2
; Sequence 2, Application US/09517739
; Patent No. 6307023
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHIO
; APPLICANT: KAISHO, NISHINOMIYA
; TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
; PRE-B CELL GROWTH-SUPPORTING ABILITY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/517,739
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,252
; FILING DATE: 23-DEC-1997
; APPLICATION NUMBER: US 08/537,942
; FILING DATE: 21-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00819
; FILING DATE: 20-MAY-1994

REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4767-0005-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:

NAME/KEY: sig_peptide
; LOCATION: 1..84
; OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"

US-09-517-739-2

Query Match 1.2%; Score 19; DB 4; Length 1411;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1112 ACAGCACCCTCTGACTG 1130

DB 948 ACAGCACCCTCTGACTG 966

RESULT 4

US-08-470-179-189/c

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; Sequence 189, Application US/08470179
; Patent No. 5645994
; GENERAL INFORMATION:
; APPLICANT: Huang Ph.D, Wai Mun
; TITLE OF INVENTION: Method and Compositions for
; IDENTIFICATION OF SPECIES IN A SAMPLE
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Trask, Britt and Rossa
; STREET: P.O. Box 2550
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: USA
; ZIP: 84110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,179
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweigert Ph.D, Susan E.
; REGISTRATION NUMBER: 36,289
; REFERENCE/DOCKET NUMBER: 2601
; TELEPHONE: 801-532-1922
; TELEFAX: 801-531-9168
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Thermus thermophilus
; US-08-470-179-189

Query Match 1.0%; Score 17; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 48 GCAGGACCCCTTCCTGG 64
Db 61 GCAGGACCCCTTCCTGG 45

RESULT 5
US-08-194-981E-4
; Sequence 4, Application US/08194981E
; Patent No. 5886157
; GENERAL INFORMATION:
; APPLICANT: GUENGERICH, F. Peter
; APPLICANT: GUO, Zuyu
; APPLICANT: SANDHU, Punam
; APPLICANT: GILLAM, Elizabeth M. J.
; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF
; TITLE OF INVENTION: HUMAN
; TITLE OF INVENTION: CYTOCHROME P450
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street, NE
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,981E
; FILING DATE: February 10, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Selby
; REGISTRATION NUMBER: 38,298
; REFERENCE/DOCKET NUMBER: 22000.0022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-194-981E-4

Query Match 1.0%; Score 17; DB 2; Length 1419;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1266 GTGTGGGAGAGCCCTG 1282
Db 1250 GTGTGGGAGAGCCCTG 1266

RESULT 6
US-08-660-963-9
; Sequence 9, Application US/08660963
; Patent No. 5852187
; GENERAL INFORMATION:
; APPLICANT: Thorne, Michael O.
; APPLICANT: Gaylinn, Bruce D.
; APPLICANT: Horikawa, ReiKo
; APPLICANT: Lyons Jr., Charles E.
; TITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE PITUITARY
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE RECEPTOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
; STREET: Metropolitan Square Building, Suite 800, 1450
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,963
; FILING DATE: 12-JUN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: O'Shaughnessy, Brian P.
; REGISTRATION NUMBER: 32,747
; REFERENCE/DOCKET NUMBER: 18046.036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-824-8000
; TELEFAX: 202-824-8199
; TELEX: 248516
; INFORMATION FOR SEQ ID NO: 9:
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;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1545 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..1371
US-08-660-963-9

Query Match 1.0%; Score 17; DB 2; Length 1545;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 484 GAGGCTGCTCCCTGTGCC 500
Db 478 GAGGCTGCTCCCTGTGCC 494

RESULT 7

US-09-101-146-63
; Sequence 63, Application US/09101146
; Patent No. 6124125
; GENERAL INFORMATION:
; APPLICANT: Dartmouth College, St. Vincents Institute of
; APPLICANT: Medical Research, Kemp et al.
; TITLE OF INVENTION: NO. 6124125e1 AMP Activated Protein Kinase
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053

COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101.146
; FILING DATE: October 7, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PN7450
; FILING DATE: 8 JAN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: DC-0050
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1576
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: NO

US-09-101-146-63
Query Match 1.0%; Score 17; DB 3; Length 1576;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 737 ATGCTGACCATCACTGA 753
Db 346 ATGCTGACCATCACTGA 362

RESULT 8

US-08-194-981E-3
; Sequence 3, Application US/08194981E
; Patent No. 5886157
; GENERAL INFORMATION:
; APPLICANT: GUENGERICH, F. Peter
; APPLICANT: GUO, Zuyu
; APPLICANT: SANDHU, Punam
; APPLICANT: GILLAM, Elizabeth M. J.
; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF
; TITLE OF INVENTION: HUMAN
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street, NE
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,981E
; FILING DATE: February 10, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Selby
; REGISTRATION NUMBER: 38,298
; REFERENCE/DOCKET NUMBER: 22000.0022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

US-08-194-981E-3

Query Match 1.0%; Score 17; DB 2; Length 1591;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1266 GTGTGGGAGGAGCCCTG 1282
Db 1304 GTGTGGGAGGAGCCCTG 1320

RESULT 9

US-08-646-273-18
; Sequence 18, Application US/08646273
; Patent No. 6066502
; GENERAL INFORMATION:
; APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt, Hei
; APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Hei
; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinkauff
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.0
; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646.273
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/03706
; FILING DATE: 11-NOV-1994
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1703 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA for mRNA
US-08-646-273-18

Query Match 1.0%; Score 17; DB 3; Length 1703;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 647 CTGGAGATCAAGAAGGC 663
Db 983 CTGGAGATCAAGAAGGC 999

RESULT 10
US-08-201-118-10
; Sequence 10, Application US/08201118
; Patent No. 5786191
; GENERAL INFORMATION:
; APPLICANT: GOLDSTEIN, Joyce A.
; APPLICANT: ROMKES-SPARKS, Marjorie
; TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY
; TITLE OF INVENTION: DNAs FOR MULTIPLE MEMBERS OF THE HUMAN CYTOCHROME P450 2C
; TITLE OF INVENTION: SUBFAMILY
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201.118
; FILING DATE: 22-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,962
; FILING DATE: 09-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 15280-192-1
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1852 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-08-201-118-10

Query Match 1.0%; Score 17; DB 1; Length 1852;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 GTGTGGGAGAGCCCTG 1282
Db 1314 GTGTGGGAGAGCCCTG 1330

RESULT 11
US-08-238-821B-10
; Sequence 10, Application US/08238821B
; Patent No. 5912120
; GENERAL INFORMATION:
; APPLICANT: GOLDSTEIN, Joyce A.
; APPLICANT: ROMKES-SPARKS, Marjorie
; APPLICANT: DE MORAS, Sonia M.F.
; TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
; TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF S-
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/238,821B
; FILING DATE: 06-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,118
; FILING DATE: 22-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,962
; FILING DATE: 09-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 15280-192110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 326-2400
; TELEFAX: (650) 326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1852 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..10
; OTHER INFORMATION: /note= "Corresponds to positions -10 to-1
; OTHER INFORMATION: for 65 of Figure 2."
US-08-238-821B-10

Query Match 1.0%; Score 17; DB 2; Length 1852;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 GTGTGGGAGAGCCCTG 1282
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CYTOCHROME P450

FILING DATE: 06-MAY-1994

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/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA: US 08/201,118
/ APPLICATION NUMBER: US 08/201,118
/ FILING DATE: 22-FEB-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/864,962
/ FILING DATE: 09-APR-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Liebeschuetz, Joe
/ REGISTRATION NUMBER: 37,505
/ REFERENCE/DOCKET NUMBER: 15280-192110US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 326-2400
/ TELEFAX: (650) 326-2422
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1854 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: CDNA
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..12
/ OTHER INFORMATION: /note= "Corresponds to positions -12 to-1
US-08-238-821B-4

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1266 GTGTGGGAGAGCCCTG 1282
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Db 1316 GTGTGGGAGAGCCCTG 1332

RESULT 15
PCT-US95-05744-4
/ Sequence 4, Application PC/TUS9505744
/ GENERAL INFORMATION:
/ APPLICANT: GOLDSTEIN, Joyce A.
/ APPLICANT: ROMKES-SPARKS, Marjorie
/ APPLICANT: DE MORAIS, Sonia M.F.
/ TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
/ TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
/ TITLE OF INVENTION: OF S-MEPHNYTOIN METABOLISM
/ NUMBER OF SEQUENCES: 61
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Hourie and Crew
/ STREET: 379 Lytton Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: US
/ ZIP: 94301
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/05744
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/238,821
/ FILING DATE: 06-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/201,118
/ FILING DATE: 22-FEB-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/864,962
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/ FILING DATE: 09-APR-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dow, Karen B.
/ REGISTRATION NUMBER: 29,684
/ REFERENCE/DOCKET NUMBER: 15280-192-1-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 326-2400
/ TELEFAX: (415) 326-2422
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1854 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: CDNA
PCT-US95-05744-4

Query Match          1.0%; Score 17; DB 5; Length 1854;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1266 GTGTGGGAGAGCCCTG 1282
    |||||||
Db 1316 GTGTGGGAGAGCCCTG 1332

Search completed: January 7, 2003, 20:22:20
Job time : 72.0864 secs
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According to the Pre Publication Rules, every patent application received by the United States Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

Two new databases have been created to hold the pre-published sequences:
Published_Applications_NA contains nucleic acid sequences; the search results will have the extension .rnpb.

Published_Applications_AA contains amino acid sequences; the search results will have the extension .rapb.

Each pre-published application is given a unique Publication Number. An example of a Publication Number is US20021234567A1. The "US" indicates the application was a U.S. application. The first 4 digits show the calendar year the application was published. The next 7 digits represent when the application was published. This 7-digit number starts at zero at the beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application had been published. If the applicants submit changes to the application, they may request that the changed application be published again. In such instances, the "1" at the end of the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to leave these results in the case.

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 17:17:03 ; Search time 500.908 Seconds
(without alignments)
1486.844 Million cell updates/sec

Title: US-09-826-581-3
Perfect score: 1722
Sequence: 1 cctggccctccagatcaaga.....gatgagaggctgggtgga 1722

Scoring table: OLIIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 381593 seqs, 216252194 residues

Word size : 15

Total number of hits satisfying chosen parameters: 1562

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
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11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1722	100.0	1722	10	US-09-826-581-3
2	346	20.1	378	10	US-09-864-761-3373
3	168	9.8	1647	10	US-09-826-581-5
4	65	3.8	92	10	US-09-864-761-20146
5	19	1.1	229	9	US-09-922-296-2
6	19	1.1	239	9	US-09-922-296-1
7	19	1.1	389	9	US-09-922-296-5
8	19	1.1	389	9	US-09-922-296-6
9	19	1.1	413	9	US-09-922-296-6
10	19	1.1	422	9	US-09-922-296-6
11	19	1.1	422	9	US-09-922-296-6
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C 21	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 22	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 23	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 24	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 25	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 26	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 27	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
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C 30	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 31	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 32	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 33	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 34	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 35	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
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C 37	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 38	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 39	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 40	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 41	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 42	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 43	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 44	19	1.1	422	10	US-09-989-722-362	Sequence 362, App
C 45	19	1.1	422	10	US-09-989-722-362	Sequence 362, App

ALIGNMENTS

RESULT 1
US-09-826-581-3
; Sequence 3, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1722
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-3

Query Match	100.0%	Score 1722;	DB 10;	Length 1722;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1722;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
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DB	1	CCTGGCCCTCAGATCAAGAGCCCTTTCTTCTCTGGTGGCCAAACGGTGTGGGGCAGC	60	
QY	61	CCCTCTATGGGACAGCAAGAGAGCTTTCTGGGTGAGGAGAGCTGGGAGGTGAAG	120	
DB	61	CCCTCTATGGGACAGCAAGAGAGCTTTCTGGGTGAGGAGAGCTGGGAGGTGAAG	120	
QY	121	GGAGATGGAGGAGGTGAGGGGAGATCTGTACGGTGTGTCTGGGGCTGATCTCTGATAT	180	
DB	121	GGAGATGGAGGAGGTGAGGGGAGATCTGTACGGTGTGTCTGGGGCTGATCTCTGATAT	180	
QY	181	ACCACAAAGCTTGGCTTTCAGGCCCAAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC	240	
DB	181	ACCACAAAGCTTGGCTTTCAGGCCCAAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC	240	

;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 3373
;; LENGTH: 378
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC009974.3
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.9
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
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;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
US-09-864-761-3373

Query Match 20.1%; Score 346; DB 10; Length 378;
Best Local Similarity 100.0%; Pred. No. 4.2e-159;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCCTCAGATCAAGAAGCCCTTTCTGCTCTGTGGCCCAACGGTGTGGGGCAGC 60
|||||
Db 362 CTTGGCCCTCAGATCAAGAAGCCCTTTCTGCTCTGTGGCCCAACGGTGTGGGGCAGC 303
QY 61 CCTCTATGGACAGCAAGACAGAGCTTTGTGGGTGAGGAGAGCTGGGAGGTGAAG 120
|||||
Db 302 CCTCTATGGACAGCAAGACAGAGCTTTGTGGGTGAGGAGAGCTGGGAGGTGAAG 243
QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 180
|||||
Db 242 GGAGATGGAGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 183
QY 181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 240
|||||
Db 182 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 123
QY 241 GGAGTCTGCATGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
|||||
Db 122 GGAGTCTGCATGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63
QY 301 ATGACCAGCTGACACCTTTTACCTCCGCTACTGCATGGCCCTGTGC 346
|||||
Db 62 ATGACCAGCTGACACCTTTTACCTCCGCTACTGCATGGCCCTGTGC 17

RESULT 3
US-09-826-581-5
; Sequence 5, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, U. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1647
; TYPE: DNA

;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (20)....(1486)
US-09-826-581-5

Query Match 9.8%; Score 168; DB 10; Length 1647;
Best Local Similarity 100.0%; Pred. No. 3.1e-72;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1523 GGTTCCTCTGTCGCCCGCCCTCTCTCTACCGCACTATCCAAGATTTGGGCATCGC 1582
|||||
Db 1022 GGTTCCTCTGTCGCCCGCCCTCTCTCTACCGCACTATCCAAGATTTGGGCATCGC 1081
QY 1583 ACATTCCGAGACTTGGCTGTGGTCTGGAGACAGCACCCTCTGACTGCACTGGACATC 1642
|||||
Db 1082 ACATTCCGAGACTTGGCTGTGGTCTGGAGACAGCACCCTCTGACTGCACTGGACATC 1141
QY 1643 TTTGTGACCGGCGTGTCTGCACTGCCTGTGGTCAACGAATGTGGT 1690
|||||
Db 1142 TTTGTGACCGGCGTGTCTGCACTGCCTGTGGTCAACGAATGTGGT 1189

RESULT 4

US-09-864-761-20146/c
; Sequence 20146, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:

;; APPLICANT: Penn, Sharron G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: Aemica-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29

```

; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20146
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009974.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
; OTHER INFORMATION: NT HIT: g11430152, EVALUE 2.00e-22
; OTHER INFORMATION: EST_HUMAN HIT: BE327467.1, EVALUE 3.00e-06
; OTHER INFORMATION: SWISSPROT HIT: P54619, EVALUE 3.00e-03
US-09-864-761-20146

```

```

Query Match      3.8%; Score 65; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.3e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CTTGGCCCTCAGATCAAGAAGCCCTTCTTTGCTCTGGTGCCACGGGTGTCGGGCAGC 60
      |||||||
Db 65 CTTGGCCCTCAGATCAAGAAGCCCTTCTTTGCTCTGGTGCCACGGGTGTCGGGCAGC 6

```

```

QY 61 CCCTC 65
      |||||
Db 5 CCCTC 1

```

```

RESULT 5
US-09-864-761-27246
; Sequence 27246, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663

```

```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27246
; LENGTH: 190
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004108.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.75
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.78
; OTHER INFORMATION: SWISSPROT HIT: P32595, EVALUE 7.60e-01
; OTHER INFORMATION: NT HIT: AF146793.2, EVALUE 4.40e-01
; OTHER INFORMATION: EST_HUMAN HIT: BE300286.1, EVALUE 1.70e-01
US-09-864-761-27246

```

```

Query Match      1.1%; Score 19; DB 10; Length 190;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1232 CATCTGTGCAGCCCTGTTTG 1250
      |||||||
Db 90 CATCTGTGCAGCCCTGTTTG 108

```

```

RESULT 6
US-09-092-296-2/c
; Sequence 2, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

```

```
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-092-296-2
```

```
Query Match 1.1%; Score 19; DB 9; Length 229;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 116 TGAAGGAGATGGAGGAGG 134
|||
Db 222 TGAAGGAGATGGAGGAGG 204
```

```
RESULT 7
US-09-092-296-1/c
; Sequence 1, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL USA
; COUNTRY: IL USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 base pairs
; TYPE: nucleic acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: base_polymorphism
; LOCATION: 200
; OTHER INFORMATION: /note= " N' represents an A or G or
; OTHER INFORMATION: T or C polymorphism at this position"
; US-09-092-296-1
```

```
Query Match 1.1%; Score 19; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 TGAAGGAGATGGAGGAGG 134
|||
Db 226 TGAAGGAGATGGAGGAGG 208
```

```
RESULT 8
US-09-092-296-5/c
; Sequence 5, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-092-296-5
```

```
Query Match 1.1%; Score 19; DB 9; Length 389;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 TGAAGGAGATGGAGGAGG 134
```



```
Db 196 TGAAGGAGATGGAGG 178
|||||
RESULT 9
US-09-092-296-6/c
; Sequence 6, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-092-296-6
Query Match 1.1%; Score 19; DB 9; Length 413;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 TGAAGGAGATGGAGG 134
|||||
Db 223 TGAAGGAGATGGAGG 205
|||||
RESULT 10
US-09-992-598-362/c
; Sequence 362, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
```

```
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; ACIDS ENCODING THE SAME
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
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; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.1%; Score 19; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 TGAAGGAGATGGAGGAGG 134
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Db 234 TGAAGGAGATGGAGGAGG 216

RESULT 11

US-09-989-293A-362/c
; Sequence 362, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney,Austin L.
APPLICANT: Kljavin,Ivar J.
APPLICANT: Napier,Mary A.
APPLICANT: Pan,James
APPLICANT: Paoni,Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.1%; Score 19; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 15;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 116 TCAAGGGAGATGGAGGAGG 134
Db 234 TCAAGGGAGATGGAGGAGG 216

RESULT 12

US-10-063-547-65/c
; Sequence 65, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2230R1C1
; CURRENT APPLICATION NUMBER: US/10/063.547
; PRIOR FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 65
; LENGTH: 422
; TYPE: DNA

i ORGANISM: Homo Sapien
US-10-063-547-65

Query Match 1.1%; Score 19; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 116 TCAAGGGAGATGGAGGAGG 134
Db 234 TCAAGGGAGATGGAGGAGG 216

RESULT 13

US-09-989-735-362/c
; Sequence 362, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C61
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; CURRENT FILING DATE: 2001-11-19
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64	PRIOR FILING DATE: 1998-07-07
65	PRIOR APPLICATION NUMBER: 60/092182
66	PRIOR FILING DATE: 1998-07-09

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QY 116 TCAAGGAGATCGAGGAGG 134
 Db 234 TCAAGGAGATCGAGGAGG 216

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US-09-990-444-362/c
 ; Sequence 362, Application US/09990444
 ; Publication No. US20020193300A1
 ; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Klijavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C19
 ; CURRENT APPLICATION NUMBER: US/09/990,444
 ; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1998-07-09
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Query Match 1.1%; Score 19; DB 9; Length 422;

Best Local Similarity 100.0%; Pred. No. 15; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 116 TGAAGGGAGATGGAGGAGG 134

Db 234 TGAAGGGAGATGGAGGAGG 216

RESULT 15

US-09-989-730-362/c

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; Sequence 362, Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC69
; CURRENT APPLICATION NUMBER: US/09/989,730
; CURRENT FILING DATE: 2001-11-20
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.1%; Score 19; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 TGAAGGGAGATGGAGG 134
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Db 234 TGAAGGGAGATGGAGG 216

Search completed: January 7, 2003, 20:17:30
Job time : 506.908 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 09:44:42 ; Search time 2203.49 Seconds
(without alignments)
12656.598 Million cell updates/sec

Title: US-09-826-581-3
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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 15

Total number of hits satisfying chosen parameters: 56052

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	4.2	413	9	AA178898
2	38	2.2	572	13	BI344527
3	25	1.5	544	10	AW812866
4	25	1.5	576	10	AW812884
5	25	1.5	632	10	AW812763
6	25	1.5	655	10	AW812747

7	25	1.5	661	10	AW812746
8	24	1.4	458	17	AZ293182
9	24	1.4	461	10	BE126712
10	24	1.4	595	13	BM487789
11	24	1.4	636	12	BG711637
12	24	1.4	687	9	AJ451523
13	24	1.4	758	9	AJ396118
14	23	1.3	386	17	AQ926533
15	23	1.3	548	13	BI775360
16	22	1.3	258	10	BB538859
17	22	1.3	271	10	BB176083
18	22	1.3	660	17	B93026
19	22	1.3	799	17	AQ291862
20	21	1.2	180	9	AA250110
21	21	1.2	214	9	AI789929
22	21	1.2	219	10	BE667622
23	21	1.2	265	14	BQ569108
24	21	1.2	283	10	BE226658
25	21	1.2	286	10	BB527609
26	21	1.2	289	14	BQ570161
27	21	1.2	300	9	AA170921
28	21	1.2	308	10	BE667621
29	21	1.2	328	9	AV161169
30	21	1.2	333	12	BE848292
31	21	1.2	341	9	AA285611
32	21	1.2	345	9	AA981924
33	21	1.2	368	9	AA030629
34	21	1.2	368	12	BF149528
35	21	1.2	387	9	AA637403
36	21	1.2	396	9	AA444453
37	21	1.2	399	9	AA790002
38	21	1.2	399	14	W44300
39	21	1.2	400	9	AL364224
40	21	1.2	408	9	AA221662
41	21	1.2	411	12	BF780536
42	21	1.2	414	13	BI28511
43	21	1.2	417	10	BB687832
44	21	1.2	419	9	AU042711
45	21	1.2	419	9	AA271391

ALIGNMENTS

RESULT 1
AA178898
LOCUS
DEFINITION
z38d10.r1 Stratagene muscle 937209 Homo sapiens cDNA clone
IMAGE:611731 5' similar to SW:AAKG_RAT_P80385 5'-AMP-ACTIVATED
PROTEIN KINASE, GAMMA CHAIN ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AA178898.1 GI:1760259

AA178898

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 413)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,

Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin

J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,

White, Y., Wyllie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project

Unpublished (1997)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estowatson.wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1280 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 255.

FEATURES

source
Location/Qualifiers
1..413
/organism="Homo sapiens"
/db_xref="GDB:4643570"
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/clone_lib="IMAGE:611731"
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/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skeletal muscle; Vector: pBluescript SK-;
Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally.
Primer: Oligo dT. Skeletal muscle from patient with
malignant hyperthermia. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; ~5 adaptor sequence: 5' GAATTCGGCAG
3' ~3' adaptor sequence: 5' CTCAGTTTTTTTTTTTTTTT 3'"

BASE COUNT 80 a 109 c 117 g 102 t 5 others

ORIGIN

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Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1543 CTCCTCTCTACCGCACTATCCAGATTGGGCATCGGCACATTCGAGACTTGGCTGT 1602
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QY 1603 GGTGCTGGAGACA 1615
Db 61 GGTGCTGGAGACA 73

RESULT 2

BI344527
LOCUS BI344527 572 bp mRNA linear EST 30-JUL-2001
DEFINITION 373008 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BI344527
VERSION BI344527.1 GI:15037807
KEYWORDS EST.
SOURCE pig.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 572)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Caeas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
and Keefe, J.W.

Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine

Unpublished (2000)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCAGACG

Plate: 119 row: I column: 11

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

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FEATURES

source
Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="ST0186"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 155 a 112 c 139 g 138 t

ORIGIN

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 CCTGGGGTCAATTTCCCATCTCT 291

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: Sall;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 106 a 190 c 151 g 124 t 1 others

ORIGIN

Query Match 2.2%; Score 38; DB 13; Length 572;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1562 ATCCAAGATTGGGCATCGGCACATTCGAGACTTGGC 1599
Db 223 ATCCAAGATTGGGCATCGGCACATTCGAGACTTGGC 260

RESULT 3

AW812866
LOCUS AW812866 544 bp mRNA linear EST 17-MAY-2000
DEFINITION RC3-ST0186-300100-017-b03 ST0186 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW812866
VERSION AW812866.1 GI:7905860
KEYWORDS EST.
SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 544)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, P., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC3-ST0186-300
100-017-b03&t3=2000-01-30&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 33

High quality sequence stop: 542.

FEATURES

source

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Db 473 CCTGGGGCTCAATTTCCCATCTGT 497
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RESULT 4
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DEFINITION
RC3-ST0186-300100-017-h03 ST0186 Homo sapiens cDNA, mRNA sequence.
ACCESSION
AWB12884
VERSION
AWB12884.1 GI:7905878
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 576)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC3-ST0186-181
00-017-h03&t3=2000-01-30&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 576.
FEATURES
source
location/Qualifiers
1..576
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0186"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 160 a 125 c 142 g 149 t
ORIGIN
Query Match 1.5%; Score 25; DB 10; Length 576;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 267 CCTGGGGCTCAATTTCCCATCTGT 291
|||||
Db 445 CCTGGGGCTCAATTTCCCATCTGT 469
|||||
RESULT 5
AWB12763
LOCUS
DEFINITION
RC3-ST0186-181099-012-h08 ST0186 Homo sapiens cDNA, mRNA sequence.
ACCESSION
AWB12763
VERSION
AWB12763.1 GI:7905757
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 655)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC3-ST0186-300
100-017-h03&t3=2000-01-30&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 576.
FEATURES
source
location/Qualifiers
1..576
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0186"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 160 a 125 c 142 g 149 t
ORIGIN
Query Match 1.5%; Score 25; DB 10; Length 576;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 267 CCTGGGGCTCAATTTCCCATCTGT 291
|||||
Db 445 CCTGGGGCTCAATTTCCCATCTGT 469
|||||
RESULT 6
AWB12747
LOCUS
DEFINITION
RC3-ST0186-181099-012-d11 ST0186 Homo sapiens cDNA, mRNA sequence.
ACCESSION
AWB12747
VERSION
AWB12747.1 GI:7905741
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 655)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
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Contact: Simpson A.J.G.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC3-ST0186-181
099-012-h08&t3=1999-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 630.
FEATURES
source
location/Qualifiers
1..632
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0186"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 169 a 145 c 157 g 160 t
ORIGIN
Query Match 1.5%; Score 25; DB 10; Length 632;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 267 CCTGGGGCTCAATTTCCCATCTGT 291
|||||
Db 437 CCTGGGGCTCAATTTCCCATCTGT 461
|||||
RESULT 7
AWB12747
LOCUS
DEFINITION
RC3-ST0186-181099-012-d11 ST0186 Homo sapiens cDNA, mRNA sequence.
ACCESSION
AWB12747
VERSION
AWB12747.1 GI:7905741
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 655)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC3-ST0186-181
099-012-h08&t3=1999-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 630.
FEATURES
source
location/Qualifiers
1..632
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0186"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 169 a 145 c 157 g 160 t
ORIGIN
Query Match 1.5%; Score 25; DB 10; Length 632;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 267 CCTGGGGCTCAATTTCCCATCTGT 291
|||||
Db 437 CCTGGGGCTCAATTTCCCATCTGT 461
|||||

```

JOURNAL
MEDLINE
COMMENT

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC3-ST0186-181
099-012-d10et3=1999-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 636.
Location/Qualifiers

FEATURES

source

1. .655
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0186"
/dev_stage="Adult"

/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 179 a 146 c 159 g 171 t

ORIGIN

Query Match 1.5%; Score 25; DB 10; Length 655;
Best Local Similarity 100.0%; Pred. No. 2.6; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 267 CCTGGGGCTCAATTTCCTCCATCTGT 291
|||||

Db 447 CCTGGGGCTCAATTTCCTCCATCTGT 471
|||||

RESULT 7

AW812746

LOCUS AW812746 661 bp mRNA linear EST 17-MAY-2000
DEFINITION RC3-ST0186-181099-012-d10 ST0186 Homo sapiens cDNA, mRNA sequence.

ACCESSION

AW812746

VERSION AW812746.1 GI:7905740

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 661)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

M.J., Soares,F., Brentani,R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shogun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC3-ST0186-181
099-012-d10et3=1999-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 661.
Location/Qualifiers

FEATURES

source

1. .661
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0186"
/dev_stage="Adult"

/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 177 a 148 c 165 g 171 t

ORIGIN

Query Match 1.5%; Score 25; DB 10; Length 661;
Best Local Similarity 100.0%; Pred. No. 2.6; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 267 CCTGGGGCTCAATTTCCTCCATCTGT 291
|||||

Db 453 CCTGGGGCTCAATTTCCTCCATCTGT 477
|||||

RESULT 8

AZ293182

LOCUS

DEFINITION

AZ293182

ACCESSION

AZ293182

VERSION

AZ293182.1 GI:9534967

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 458)

Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret

B., Levis,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.

and Fraser,C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other GSSs: RPCI-23-159017-TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tldb/bacends/mouse/bac_end_intro.html

Plate: 159 row: 0 column: 17

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1. .458

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-159017"

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/clone_lib="RPCL-23"
/sex="Female"
/lab_host="DH10B"
/Note="Organ: Kidney/Brain; Vector: pBACe3.6; Site: 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI MethyIase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)".
BASE COUNT      142 a      74 c      117 g      125 t
ORIGIN

Query Match
Best Local Similarity 1.4%; Score 24; DB 17; Length 458;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 GGGGAGGTGAAGGAGATGGAGCA 132
Db 41 GGGGAGGTGAAGGAGATGGAGCA 64

RESULT 9
BE126712
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

BE126712
DEPA0460 Rat Lambda ZAP Express Library Rattus norvegicus cDNA 5',
mRNA sequence.
BE126712
BE126712.1 GI:8549403
EST.
SOURCE
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 461)
Sleeman,M.A., Murison,J.G., Strachan,L., Kumble,K.D., Glenn,M.P.,
McGrath,A., Grierson,A., Havukkala,I., Tan,P.L.U. and Watson,J.D.
Expressed sequence tags of cDNA clones from rat dermal papilla
cells
Unpublished (2000)
Contact: Sleeman MA
Biology
Genesis Research and Development Corporation Limited
P.O. Box 50, 1 Fox St, Parnell, Auckland, New Zealand
Tel: 0064 9 373 5600
Fax: 0064 9 373 2189
Email: m.sleeman@genesis.co.nz
Seq primer: T3 forward
High quality sequence stop: 461.
Location/Qualifiers
1..461
/organism="Rattus norvegicus"
/strain="Dark-Agouti"
/db_xref="taxon:10116"
/clone_lib="Rat Lambda ZAP Express Library"
/tissue_type="vibrissae"
/cell_type="dermal papilla"
BASE COUNT      117 a      114 c      109 g      121 t
ORIGIN

Query Match
Best Local Similarity 1.4%; Score 24; DB 10; Length 461;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 555 ATGCTGACCATCATCTGACTTCATC 578
Db 246 ATGCTGACCATCATCTGACTTCATC 269

RESULT 10
BM487789
LOCUS

```

Phasianinae; Gallus.

1 (bases 1 to 636)

Burnside, J., Morgan, R.W. and Cogburn, L.A.

Chicken ESTs from a normalized liver library

Unpublished (2001)

Contact: Joan Burnside

Molecular Endocrinology

University of Delaware

40 Townsend Hall, Newark, DE 19717, USA

Tel: 302-831-1345

Fax: 302-831-3411

Email: joan@udel.edu, www.chickest.udel.edu.

FEATURES

source

1. 636

/organism="Gallus gallus"

/db_xref="taxon:9031"

/clone="pglin.pk008.c13"

/clone_lib="Normalized Liver Library"

/sex="Male and Female"

/tissue type="liver"

/lab host="E.coli EMDH108"

/note="vector: pCMVSPORT 6"

BASE COUNT 129 a 215 c 167 g 119 t 6 others

ORIGIN

Query Match 1.4%; Score 24; DB 12; Length 636;

Best Local Similarity 100.0%; Pred. No. 7.3;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 555 ATGCTGACCATCACTGACTTCATC 578

|||||

Db 286 ATGCTGACCATCACTGACTTCATC 309

|||||

RESULT 12

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 687)

Buerstedde, J.M.

Gallus gallus bursal lymphocyte EST

Unpublished (2002)

Contact: Buerstedde JM

Cellular Immunology

Heinrich-Pette-Institute

Marinistr. 52, 20251 Hamburg, Germany

Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES

source

1. 687

/organism="Gallus gallus"

/db_xref="taxon:9031"

/clone="29a6r1"

/clone_lib="riken1"

/cell_type="bursal lymphocyte"

/dev_stage="2-3 weeks old"

/note="CB inbred strain"

BASE COUNT 143 a 228 c 191 g 125 t

ORIGIN

Query Match 1.4%; Score 24; DB 9; Length 687;

Best Local Similarity 100.0%; Pred. No. 7.5;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 555 ATGCTGACCATCACTGACTTCATC 578

|||||

Phasianinae; Gallus.

1 (bases 1 to 636)

Burnside, J., Morgan, R.W. and Cogburn, L.A.

Chicken ESTs from a normalized liver library

Unpublished (2001)

Contact: Joan Burnside

Molecular Endocrinology

University of Delaware

40 Townsend Hall, Newark, DE 19717, USA

Tel: 302-831-1345

Fax: 302-831-3411

Email: joan@udel.edu, www.chickest.udel.edu.

FEATURES

source

1. 636

/organism="Gallus gallus"

/db_xref="taxon:9031"

/clone="pglin.pk008.c13"

/clone_lib="Normalized Liver Library"

/sex="Male and Female"

/tissue type="liver"

/lab host="E.coli EMDH108"

/note="vector: pCMVSPORT 6"

BASE COUNT 129 a 215 c 167 g 119 t 6 others

ORIGIN

Query Match 1.4%; Score 24; DB 12; Length 636;

Best Local Similarity 100.0%; Pred. No. 7.3;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 555 ATGCTGACCATCACTGACTTCATC 578

|||||

Db 286 ATGCTGACCATCACTGACTTCATC 309

|||||

RESULT 12

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 687)

Buerstedde, J.M.

Gallus gallus bursal lymphocyte EST

Unpublished (2002)

Contact: Buerstedde JM

Cellular Immunology

Heinrich-Pette-Institute

Marinistr. 52, 20251 Hamburg, Germany

Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES

source

1. 687

/organism="Gallus gallus"

/db_xref="taxon:9031"

/clone="29a6r1"

/clone_lib="riken1"

/cell_type="bursal lymphocyte"

/dev_stage="2-3 weeks old"

/note="CB inbred strain"

BASE COUNT 143 a 228 c 191 g 125 t

ORIGIN

Query Match 1.4%; Score 24; DB 9; Length 687;

Best Local Similarity 100.0%; Pred. No. 7.5;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 555 ATGCTGACCATCACTGACTTCATC 578

|||||

Fax: 301 838 0208
 Email: szhac@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
 Plate: 256 row: O column: 16
 Seq primer: SP6
 Class: BAC ends.

FEATURES

source
 Location/Qualifiers
 1..386
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-256O16"
 /clone_lib="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 119 a 74 c 104 g 89 t
 ORIGIN

Query Match 1.3%; Score 23; DB 17; Length 386;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 GGGAGGTGAAGGAGATGGAGGA 132
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 Db 48 GGGAGGTGAAGGAGATGGAGGA 70

RESULT 15
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 DEFINITION 467815 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BI775360
 VERSION BI775360.1 GI:15776346
 KEYWORDS EST.
 SOURCE COW.
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 1 (bases 1 to 548)
 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
 JOURNAL Genome Res. 11 (4), 626-630 (2001)
 MEDLINE 21180013

COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390

Email: smith@mail.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers
 FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGTCACGACG

Plate: 90 row: I column: 16
 Seq primer: ATTAGGTGACACTATAG.

FEATURES

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 Location/Qualifiers
 1..548
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC 2B0V"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
 Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
 BASE COUNT 119 a 173 c 163 g 93 t
 ORIGIN

Query Match 1.3%; Score 23; DB 13; Length 548;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CAGATCAAGAAGGCTTCTTTGC 33
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 Db 487 CAGATCAAGAAGGCTTCTTTGC 509

Search completed: January 6, 2003, 11:07:53
 Job time : 2212.49 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 20:16:02 ; Search time 64.9136 Seconds
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Perfect score: 1722
Sequence: 1 cctggccctcagatcaaga.....gatgagagctgggtgga 1722

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 15

Total number of hits satisfying chosen parameters: 989

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	19	1.1	1411	1	US-08-537-942A-2
3	19	1.1	1411	4	US-08-997-252A-2
4	19	1.1	1411	4	US-09-517-739-2
C 5	19	1.1	2532	4	US-09-361-631-4
C 6	19	1.1	2993	4	US-09-361-631-3
C 7	19	1.1	40352	3	US-08-846-111D-15
C 8	19	1.1	40352	4	US-09-443-077-15
9	18	1.0	511	4	US-09-404-879A-68
C 10	18	1.0	740	4	US-09-342-681C-99
C 11	18	1.0	2838	4	US-08-246-489-1
C 12	18	1.0	3691	4	US-09-211-704A-3
C 13	18	1.0	3695	4	US-09-211-704A-1
14	18	1.0	5769	1	US-08-552-971-1
15	18	1.0	5769	2	US-08-991-258A-1
16	18	1.0	5769	2	US-08-769-399-1
17	18	1.0	5769	3	US-08-991-953A-1
18	18	1.0	9096	4	US-09-147-119-5
19	18	1.0	15936	4	US-09-147-119-1
20	17	1.0	495	1	US-08-215-805A-81
C 21	17	1.0	678	3	US-09-195-286-3
C 22	17	1.0	682	4	US-09-404-879A-52
C 23	17	1.0	692	4	US-09-404-879A-15
C 24	17	1.0	699	3	US-09-195-286-2
25	17	1.0	864	1	US-08-396-650-2
26	17	1.0	864	1	US-08-768-626-2
27	17	1.0	921	1	US-08-396-650-3

28 17 1.0 921 1 US-08-396-650-4 Sequence 4, Appli
29 17 1.0 921 1 US-08-768-626-3 Sequence 3, Appli
30 17 1.0 921 1 US-08-768-626-4 Sequence 4, Appli
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C 32 17 1.0 1001 4 US-09-641-638-525 Sequence 525, App
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C 34 17 1.0 1384 2 US-08-162-402B-1 Sequence 1, Appli
35 17 1.0 1576 3 US-09-101-146-63 Sequence 63, Appli
36 17 1.0 1634 3 US-09-072-384-1 Sequence 1, Appli
37 17 1.0 1656 3 US-09-072-384-14 Sequence 14, Appli
38 17 1.0 1679 3 US-09-072-384-17 Sequence 17, Appli
C 39 17 1.0 1743 3 US-08-665-258-20 Sequence 20, Appli
C 40 17 1.0 1743 3 US-08-762-500-20 Sequence 20, Appli
C 41 17 1.0 1934 2 US-08-162-402B-7 Sequence 7, Appli
42 17 1.0 1937 3 US-08-888-949-15 Sequence 15, Appli
43 17 1.0 1937 4 US-08-888-950-15 Sequence 15, Appli
44 17 1.0 1937 4 US-09-262-758-15 Sequence 15, Appli
C 45 17 1.0 1974 3 US-08-762-500-78 Sequence 78, Appli

ALIGNMENTS

RESULT 1
US-07-853-913-1/c
; Sequence 1, Application US/07853913
; Patent No. 5338839
; GENERAL INFORMATION:
; APPLICANT: McKay, Ronald D.G.
; APPLICANT: Lendahl, Urban
; TITLE OF INVENTION: Nestin Expression As An Indicator of
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/853,913
FILING DATE: 19920319
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/660,412
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,803
FILING DATE: 25-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,762
FILING DATE: 02-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/180,548
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/POCKET NUMBER: MIT-4641AAAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11236 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-07-853-913-1

Query Match 1.1%; Score 24; DB 1; Length 11236;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7635 CTCTTTTCGAGAGATCTACCTGC 7612
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RESULT 2

US-08-537-942A-2
; Sequence 2, Application US/08537942A
; Patent No. 5753464
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHIO
; APPLICANT: KAISHO, NISHINOMIYA
; TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,942A
; FILING DATE: 21-NOV-1995

CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00819

FILING DATE: 20-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-141178

FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4767-004-0 PCT

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

MOLECULE TYPE: cdna to mRNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..84

OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"
; US-08-537-942A-2

Query Match 1.1%; Score 19; DB 1; Length 1411;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 948 ACAGCACCCTCTGACTG 966
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RESULT 3

US-08-997-252A-2
; Sequence 2, Application US/08997252A
; Patent No. 6232453
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHIO
; APPLICANT: KAISHO, NISHINOMIYA
; TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,252A
; FILING DATE: 23-DEC-1997

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/537,942

FILING DATE: 21-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00819

FILING DATE: 20-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-141178

FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4767-0005-0 PCT

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

MOLECULE TYPE: cdna to mRNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..84

OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"
; US-08-997-252A-2

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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1613 ACAGCACCCTCTGACTG 1631
|||||

Db 948 ACAGCACCCTCTGACTG 966
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RESULT 4

US-09-517-739-2
; Sequence 2, Application US/09517739
; Patent No. 6307023
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHIO
; APPLICANT: KAISHO, NISHINOMIYA

;; TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
;; TITLE OF INVENTION: PRE-B CELL GROWTH-SUPPORTING ABILITY
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; ADDRESSEE: P.C.
;; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;; CITY: ARLINGTON
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/517,739
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/997,252
;; FILING DATE: 23-DEC-1997
;; APPLICATION NUMBER: US 08/537,942
;; FILING DATE: 21-NOV-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/JP94/00819
;; FILING DATE: 20-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 5-141178
;; FILING DATE: 21-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OBLON, NORMAN F.
;; REGISTRATION NUMBER: 24,618
;; REFERENCE/DOCKET NUMBER: 4767-0005-0 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-413-3000
;; TELEFAX: 703-413-2420
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1411 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; FEATURE:
;; NAME/KEY: sig peptide
;; LOCATION: 1..84
;; OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"
US-09-517-739-2

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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1613 ACAGCACCCTCTGACTG 1631
Db 948 ACAGCACCCTCTGACTG 966

RESULT 5
US-09-361-631-4/c
; Sequence 4, Application US/09361631
; Patent No. 6383778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; FILE REFERENCE: 02307E-08872005
; CURRENT APPLICATION NUMBER: US/09/361,631

;; CURRENT FILING DATE: 1999-07-27
;; EARLIER APPLICATION NUMBER: US 60/095,464
;; EARLIER FILING DATE: 1998-07-28
;; EARLIER APPLICATION NUMBER: US 60/112,747
;; EARLIER FILING DATE: 1998-12-17
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 4
;; LENGTH: 2532
;; TYPE: DNA
;; ORGANISM: Mus sp.
;; FEATURE:
;; OTHER INFORMATION: mouse G-protein coupled receptor (GPCR) B4
;; OTHER INFORMATION: nucleotide sequence
US-09-361-631-4

Query Match 1.1%; Score 19; DB 4; Length 2532;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 119 AGGAGATGGAGGAGTGA 137
Db 2339 AGGAGATGGAGGAGTGA 2321

RESULT 6
US-09-361-631-3/c
; Sequence 3, Application US/09361631
; Patent No. 6383778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02307E-08872005
; CURRENT APPLICATION NUMBER: US/09/361,631
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/095,464
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: US 60/112,747
; EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2993
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat G-protein coupled receptor (GPCR) B4
; OTHER INFORMATION: nucleotide sequence
US-09-361-631-3

Query Match 1.1%; Score 19; DB 4; Length 2993;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 119 AGGAGATGGAGGAGTGA 137
Db 2351 AGGAGATGGAGGAGTGA 2333

RESULT 7
US-08-846-111D-15/c
; Sequence 15, Application US/08846111D
; Patent No. 6017705
; GENERAL INFORMATION:
; APPLICANT: Lurquin, Christophe; Brasseur, Francis;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
; TITLE OF INVENTION: Members Of The Mage-B Family and Uses Thereof
; NUMBER OF SEQUENCES: 18

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect For DOS 6.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846.111D
; FILING DATE: 25-APRIL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/658,578
; FILING DATE: 5-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,388
; FILING DATE: 14-MARCH-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6017705man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5444.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40352 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-846-111D-15

Query Match 1.1%; Score 19; DB 3; Length 40352;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 GGCAGGGTGGGAGGGAT 486
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Db 14949 GGCAGGGTGGGAGGGAT 14931

RESULT 8
US-09-443-077-15/C
; Sequence 15, Application US/09443077
; Patent No. 6392016
; GENERAL INFORMATION:
; APPLICANT: Lurquin, Christophe; Brasseur, Francis;
; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
; MEMBERS OF THE MAGE-8 FAMILY AND USES THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect For DOS 6.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/443,077
; FILING DATE: 26-JUN-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,111
; FILING DATE: <Unknown>
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;
; APPLICATION NUMBER: 08/403,388
; FILING DATE: 14-MARCH-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6392016man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5444.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40352 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-443-077-15

Query Match 1.1%; Score 19; DB 4; Length 40352;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14949 GGCAGGGTGGGAGGGAT 14931

RESULT 9
US-09-404-879A-68
; Sequence 68, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 68
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-404-879A-68

Query Match 1.0%; Score 18; DB 4; Length 511;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 216 GGCACGGGTGGAGGAAAG 233
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Db 248 GGCACGGGTGGAGGAAAG 265

RESULT 10
US-09-342-681C-99
; Sequence 99, Application US/09342681C
; Patent No. 6355782
; GENERAL INFORMATION:
; APPLICANT: Zonana et al.
; TITLE OF INVENTION: Hypohydrated ectodermal dysplasia genes and proteins
; FILE REFERENCE: 52978
; CURRENT APPLICATION NUMBER: US/09/342,681C
; CURRENT FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/092,279
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/112,366
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 99
LENGTH: 740
TYPE: DNA
ORGANISM: Homo sapiens
US-09-342-681C-99

Query Match 1.0%; Score 18; DB 4; Length 740;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 669 CCTCCTGGAGCCTGGTGC 686
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RESULT 11
US-08-246-489-1/c
Sequence 1, Application US/08246489
Patent No. 6225049
GENERAL INFORMATION:
APPLICANT: Lan, Michael S.
APPLICANT: No. 6225049kins, Abner L.
TITLE OF INVENTION: NOVEL HUMAN INSULINOMA-ASSOCIATED cDNA
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive
CITY: Newport Beach
STATE: California
COUNTRY: USA
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246.489
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,715
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH012.012A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2838 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: IA-1
US-08-246-489-1

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Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 12

US-09-211-704A-3/c
Sequence 3, Application US/09211704A
Patent No. 6271014
GENERAL INFORMATION:
APPLICANT: de Saint-Vis, Blandine Marie
APPLICANT: Fossiez, Francois
APPLICANT: Caux, Christophe
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Proteinases; Related Reagents
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,704A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/005,263
FILING DATE: 09-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SF0781K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 343..2028
FEATURE:
NAME/KEY: mat peptide
LOCATION: 406..2028
FEATURE:
NAME/KEY: misc feature
LOCATION: 3454

OTHER INFORMATION: /note= "nucleotide 3454 designated W, may be A or T."
US-09-211-704A-3
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Db 2389 TCCTCCCGCCCTCCCC 2372

RESULT 13
US-09-211-704A-1/c
Sequence 1, Application US/09211704A
Patent No. 6271014
GENERAL INFORMATION:
APPLICANT: de Saint-Vis, Blandine Marie
APPLICANT: Fossiez, Francois

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;
; APPLICANT: Caux, Christophe
; TITLE OF INVENTION: Mammalian Proteinases; Related Reagents
; TITLE OF INVENTION: and Methods
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/005,263
; FILING DATE: 09-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SF0781K
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3695 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
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; NAME/KEY: CDS
; LOCATION: 344..2032
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; Best Local Similarity 100.0%; Pred. No. 40;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; DB 2393 TCCTCCCGCCGCTCCCTCC 2376
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; RESULT 14
; US-08-652-971-1
; Sequence 1, Application US/08652971
; Patent No. 5814507
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.
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; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,971
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 225-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5769 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
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; LOCATION: 379..4686
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; Query Match 1.0%; Score 18; DB 1; Length 5769;
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; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 274 CTCGAATTTCCCATCTGT 291
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; RESULT 15
; US-08-991-258A-1
; Sequence 1, Application US/08991258A
; Patent No. 5928887
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/991,258A
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
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;   REGISTRATION NUMBER: 24,190
;   REFERENCE/DOCKET NUMBER: A-63478-3/WH/D/MTK
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 781-1989
;   TELEFAX: (415) 398-3249
;   TELEX:
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 5769 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 379..4686
;   US-08-991-258A-1

Query Match      1.0%; Score 18; DB 2; Length 5769;
Best Local Similarity 100.0%; Pred. No. 39,
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 207.914 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 16:44:13 ; Search time 4127.03 Seconds
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 15

Total number of hits satisfying chosen parameters: 52453

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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4	1366	82.9	2109	6	AX099776	AX099776 Sequence
5	1332	80.9	2290	9	HS2429977	AJ249977 Homo sapi
6	406	24.7	989	6	AX281579	AX281579 Sequence
7	285	17.3	206854	9	AC009974	AC009974 Homo sapi
8	278	16.9	1014	6	AX281581	AX281581 Sequence
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ALIGNMENTS

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DEFINITION Sequence 5 from Patent WO0177305.
ACCESSION AX281582
VERSION AX281582.1 GI:16608833
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Andersson,L., Luthman,H. and Marklund,S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL Patent: WO 0177305-A 5 18-OCT-2001;

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RESULT 2
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DEFINITION Sequence 29 from Patent WO0120003.
ACCESSION AX099802
VERSION AX099802.1 GI:13538836
KEYWORDS linear PAT 02-APR-2001

SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2115)
AUTHORS Anderson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and Chardon,P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
JOURNAL Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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BASE COUNT 460 a 622 c 562 g 471 t
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Best Local Similarity 99.9%; Pred. No. 0;
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DB 61 TCAGAAAGAAATCCGTGGGAAACCGAGGCGCCAAAGCCTTTGAGATGGACAGCAAGTCG 120
QY 215 GTGAGGAAAGGGAGCCACACAGGTACAGGGAAGGTCCCGGTCCAGGCCAGCTGCTGAG 274
DB 121 GTGAGGAAAGGGAGCCACACAGGTACAGGGAAGGTCCCGGTCCAGGCCAACTGCTGAG 180
QY 275 TCCACCGGCTGGAGGCCACATCCCAAGACCAACACCTTGGCTCAAGCTGATCCTGCC 334
DB 181 TCCACCGGCTGGAGGCCACATCCCAAGACCAACACCTTGGCTCAAGCTGATCCTGCC 240
QY 335 GGGTGGGCACTCCACCAACAGGTGGGACTGCCTCCCTCTGACTGTACAGCCTCAGCT 394
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DB 1381 GCCTCGGGGCTTGAGAAGATCTGAGTCTCAATCCCAAGCCA 1423

RESULT 3
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LOCUS
DEFINITION Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
mRNA, complete cds.
ACCESSION AF214519
VERSION AF214519.1 GI:8215681
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RESULT 4	AX099776	Sequence 3 from Patent WO0120003.	2109 bp	DNA	linear	PAT 02-APR-2001
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DEFINITION	AX099776	Sequence 3 from Patent WO0120003.				
ACCESSION	AX099776	Sequence 3 from Patent WO0120003.				
VERSION	AX099776.1	GI:13538810				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	1	(bases 1 to 2109)				
AUTHORS	Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and Chardon, P.					
TITLE	variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof					
JOURNAL	PATENT: WO 0120003-A 3 22-MAR-2001; INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ; Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)					
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BASE COUNT	458 a 621 c 560 g 470 t					
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Db	181	GGGCTGGAGGCCACATTCGCCACAGACCACACCTTGCTGCTCAAGCTGATCTCGCGGGTG	240			
Qy	341	GGCACTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTACAGCCTCAGCTGCAGGC	400			
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Qy	401	TCCAGCACAGATGATGGAGCTGGGCCACCGAGTTTCCAGCCACAGAGCCTGGGAGTGT	460			
Db	301	TCCAGCACAGATGATGGAGCTGGGCCACCGAGTTTCCAGCCACAGAGCCTGGGAGTGT	360			
Qy	461	GAGCTAGAAGCCCTGCTGGGAAGAGAGGCCCTGCCCTGTGCTGTGCCAGGCCCATTT	520			
Db	361	GAGCTAGAAGCCCTGCTGGGAAGAGAGGCCCTGCCCTGTGCTGTGCCAGGCCCATTT	420			
Qy	521	CCCAAGCTGGGCTGGGATGACAACTCGGGAACCCGGGCGCCAGATCTACATGCGCTTC	580			

ACCESSION	AJ249977
VERSION	AJ249977.1 GI:6688200
KEYWORDS	AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 2290)
REFERENCE	Cheung,P.C., Salt,I.P., Davies,S.P., Hardie,D.G. and Carling,D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding Biochem. J. 346 Pt 3, 659-669 (2000)
JOURNAL	20164049
MEDLINE	10698692
PUBMED	2 (bases 1 to 2290)
REFERENCE	Carling,D. Direct Submission Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 0NN, UNITED KINGDOM
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PUBMED	/db_xref="taxon:9606"
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AUTHORS	/gene="AMPK gamma 3"
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MEDLINE	/function="AMP-activated protein kinase regulatory subunit"
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QY	1441	TCAGGCACTGGTGTCTAGCCCTCTGTCGATCGATGCCCTCGGGCCCTGAGAACATCTGAG	1500
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QY	1501	TCCTCAATCCCAAGCCACCTGCACACCTGAAGCCAAATGAAGGAACTGAGAACTCAGC	1560
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RESULT 6			
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DEFINITION	AX281579		
ACCESSION	AX281579		
VERSION	AX281579.1	GI:16608930	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1		
JOURNAL	Anderson, L., Luthman, H. and Marklund, S.		
	Variances of the human amp-activated protein kinase gamma 3 subunit		
	Patent: WO 0177305-A 2 18-OCT-2001;		
	Arexis AB (SE)		
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QY	367	CCTCCCTCTGACTACAGCTCAGCTGACGGCTCCAGCAGACAGATGATGGAGCTGGC	426
Db	660	CCTCCCTCTGACTACAGCTCAGCTGACGGCTCCAGCAGACAGATGATGGAGCTGGC	719
QY	427	CACGAGTTCACAGCCACAGAGGCTGGGAGTGTGAGCTAGAGGCCCTGCTGGGAAGAGAG	486
Db	720	CACGAGTTCACAGCCACAGAGGCTGGGAGTGTGAGCTAGAGGCCCTGCTGGGAAGAGAG	779
QY	487	GCCTGCCCTGTGCTGTCCCGAGGCCCATTTCCCAAGCTGGGCTGGGATGACGAACT	546
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QY	547	GCAGAAACCCGGGCCACAGATCTACATCGCTTTCATGACGAGGACACACCTGCTACGATGC	606
Db	840	GCAGAAACCCGGGCCACAGATCTACATCGCTTTCATGACGAGGACACACCTGCTACGATGC	899
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Db	900	CATGGCAACTAGCTCCAGCTAGTCTATCTTCGACACCATGCTGGAG	945
RESULT 7			
LOCUS	AC009974/C	206854 bp DNA linear PRI 09-JAN-2002	

Tateno, M., Catanesse, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. An unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

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OY 547 GCGGAAACCGCGCGCGCCAGATCTACATGCGCTTTCATGCGAGGACACCTGCTACGATGC 606
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OY 607 CATGGCAACTAGCTCAAGCTAGTATCTTTCGACACCACTGCTGGAG 652
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RESULT 8
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LOCUS AX281581 1014 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 4 from Patent WO0177305.
ACCESSION AX281581
VERSION AX281581.1 GI:16608832
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Anderson, L., Luthman, H. and Marklund, S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL Patent: WO 0177305-A 4 18-OCT-2001;
AREXIS AB (SE)
FEATURES
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/db_xref="taxon:9606"
BASE COUNT 192 a 325 c 271 g 226 t
ORIGIN

Query Match 16.9%; Score 278; DB 6; Length 1014;
Best Local Similarity 100.0%; Pred. No. 2.7e-136;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1370 CAGGTACACAGCGTGGTGCTAGTGGAGAGACCCAGCATCTTTGGCGTGTCTCCCTC 1429
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OY 1430 TCCGACATCTCTTTCAGGCACCTGCTCAGCCCTGCTGCGCATCGATCCCTCGGGCTGA 1489
Db 797 TCCGACATCTCTTTCAGGCACCTGCTCAGCCCTGCTGCGCATCGATCCCTCGGGCTGA 856

OY 1490 GAAGATCTGAGTCTCAATCCCAAGCCACCTGCACACCTGGAAGCAATGAAGGAACTG 1549
Db 857 GAAGATCTGAGTCTCAATCCCAAGCCACCTGCACACCTGGAAGCAATGAAGGAACTG 916

OY 1550 GAGAACTCAGCTTCATCTTCCCGCCACCCCATTTGCTGTTTTCAGTATGATTCAGGTAG 1609
Db 917 GAGAACTCAGCTTCATCTTCCCGCCACCCCATTTGCTGTTTTCAGTATGATTCAGGTAG 976

OY 1610 GCTTGCCTTGGGCCATGACACAGCGCTCTTAGTCTTC 1647
Db 977 GCTTGCCTTGGGCCATGACACAGCGCTCTTAGTCTTC 1014

RESULT 9
AC027416
LOCUS AC027416 152129 bp DNA linear HTG 07-JUN-2000
DEFINITION Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
unordered pieces.
ACCESSION AC027416
VERSION AC027416.2 GI:8317289
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152129)
Birten, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-504G11
Unpublished
2 (bases 1 to 152129)
Birten, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, P.,
Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Chepel, Y., Colangelo, M., Collins, S.,
Collamore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meidrim, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J.,
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O'Neill, D., Olivari, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tefaye, S., Theodore, J., Tirrell, A., Travers, M., Trifilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L7458
Center clone name: 504.G.11
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135376 bases at least Q40
Consensus quality: 143264 bases at least Q30
Consensus quality: 146503 bases at least Q20
Insert size: 161000; agarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1005: contig of 1005 bp in length
* 1006 1105: gap of 100 bp
* 1106 2402: contig of 1297 bp in length
* 2403 2502: gap of 100 bp
* 2503 3823: contig of 1321 bp in length
* 3824 3923: gap of 100 bp
* 3924 5020: contig of 1097 bp in length
* 5021 5120: gap of 100 bp
* 5121 6161: contig of 1041 bp in length
* 6162 6261: gap of 100 bp
* 6262 7547: contig of 1286 bp in length
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* 7548 7647: gap of 100 bp
* 7648 7983: contig of 2336 bp in length
* 9884 10083: gap of 100 bp
* 10084 12556: contig of 2473 bp in length
* 12557 12656: gap of 100 bp
* 12657 15043: contig of 2387 bp in length
* 15044 15143: gap of 100 bp
* 15144 17123: contig of 1980 bp in length
* 17124 17223: gap of 100 bp
* 17224 19466: contig of 2243 bp in length
* 19467 19566: gap of 100 bp
* 19567 21928: contig of 2362 bp in length
* 21929 22028: gap of 100 bp
* 22029 24319: contig of 2291 bp in length
* 24320 24419: gap of 100 bp
* 24420 27059: contig of 2640 bp in length
* 27060 27159: gap of 100 bp
* 27160 30170: contig of 3011 bp in length
* 30171 30270: gap of 100 bp
* 30271 33968: contig of 3698 bp in length
* 33969 34068: gap of 100 bp
* 34069 38179: contig of 4111 bp in length
* 38180 38279: gap of 100 bp
* 38280 42366: contig of 4087 bp in length
* 42367 42466: gap of 100 bp
* 42467 46365: contig of 3899 bp in length
* 46366 46465: gap of 100 bp
* 46466 51285: contig of 4820 bp in length
* 51286 51385: gap of 100 bp
* 51386 55871: contig of 4486 bp in length
* 55872 55971: gap of 100 bp
* 55972 60595: contig of 4624 bp in length
* 60596 60695: gap of 100 bp
* 60696 66595: contig of 5900 bp in length
* 66596 66695: gap of 100 bp
* 66696 73218: contig of 6523 bp in length
* 73219 73318: gap of 100 bp
* 73319 77115: contig of 3797 bp in length
* 77116 77215: gap of 100 bp
* 77216 85023: contig of 7807 bp in length
* 85023 85122: gap of 100 bp
* 85123 93314: contig of 8192 bp in length
* 93315 93414: gap of 100 bp
* 93415 101193: contig of 7779 bp in length
* 101194 101294: gap of 100 bp
* 101294 113090: contig of 11797 bp in length
* 113091 113190: gap of 100 bp
* 113191 123496: contig of 10306 bp in length
* 123497 123596: gap of 100 bp
* 123597 137837: contig of 14241 bp in length
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Best Local Similarity 100.0%; Score 278; DB 2; Length 152129;

Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 139718 CAGGTACACAGGCTGGTGTAGTGGACGAGACCCAGCATCTCTTGGGCGTGTCTCCCTC 139777
|||||
QY 1430 TCCGACATCTTCAGGCACCTGGTGTCTCAGCCCTGCTGGCATCGATCCCTCGGGGCTTGA 1489
|||||
Db 139778 TCCGACATCTTCAGGCACCTGGTGTCTCAGCCCTGCTGGCATCGATCCCTCGGGGCTTGA 139837
|||||
QY 1490 GAAGATCTGAGTCTCTCAATCCCAAGCCACCTGCACACCTGGAAGCCAAATGAAGGGAACCTG 1549
|||||
Db 139838 GAAGATCTGAGTCTCTCAATCCCAAGCCACCTGCACACCTGGAAGCCAAATGAAGGGAACCTG 139897
|||||
QY 1550 GAGAACTCAGCCTTTCATCTCCCCACCCCATTTGCTGGTTTCAGCTATGATTACAGGTAG 1609
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Db 139898 GAGAACTCAGCCTTTCATCTCCCCACCCCATTTGCTGGTTTCAGCTATGATTACAGGTAG 139957
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QY 1610 GCTCTGCCCTGGGCCATGACACAGCCTCTTAGTCTTC 1647
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RESULT 10
AC027416/c

AC027416 152129 bp DNA linear HTG 07-JUN-2000
Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
unordered pieces.
AC027416
AC027416.2 GI:8317289
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152129)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-504G11
Unpublished
2 (bases 1 to 152129)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boquelavsky,L., Bouckgalter,B., Brown,A., Burkett,G.,
Campiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,D., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRoque,K., Lanazares,R., Landers,T., Lechoczky,J.,
Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
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O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrelli,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L7458
Center clone name: 504_G_11
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135376 bases at least Q40
Consensus quality: 143284 bases at least Q30
Consensus quality: 146503 bases at least Q20
Insert size: 161000; agarose-fp
Insert size: 149029; sum-of-ctngs
Quality coverage: 3.1 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-ctngs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1005: contig of 1005 bp in length
* 1006 1105: gap of 100 bp

Denaturation: 94 degrees C for 30 seconds
Annealing: 55 degrees C for 30 seconds
Polymerization: 72 degrees C for 30 seconds
PCR cycles: 33
Thermal cycler: Perkin Elmer 9600
Protocol:

Template: 25 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: 0.1 units/reaction
Total Vol: 15 ul

Buffer:

MgCl2: 2 mM
KCl: 50 mM
Tris-HCL: 20 mM
pH: 8.4

Primers were defined on sequence AAl78898 (cDNA). No intron.

FEATURES
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/clone_lib="Human"

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Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 50 ATCTGACTGCACATCTTTGGACCGCGGTGCTGTCACATGCTGTGGTC 106

RESULT 13
AX281578
LOCUS
DEFINITION
Sequence 1 from Patent WO0177305.
ACCESSION
AX281578
VERSION
AX281578.1 GI:16608929
KEYWORDS
SOURCE
human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS
Andersson, L., Luchman, H. and Marklund, S.
TITLE
Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL
Patent: WO 0177305-A 1 18-OCT-2001;
Arexis AB (SE)

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BASE COUNT 139 a 219 c 259 g 204 t

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Best Local Similarity 100.0%; Pred. No. 8.6e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 313 TTGGTCTGGGCTGCCACATGACCGCGGCTGGAGCAGCAGCTGGCGAGG 364

RESULT 14
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LOCUS
DEFINITION
Sequence 1 from Patent WO0120003.
ACCESSION
AX099774
VERSION
AX099774.1 GI:13538808
KEYWORDS
SOURCE
pig.
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 1867)
AUTHORS
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., Le Roy, P. and Chardon, P.
TITLE
Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
JOURNAL
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)

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BASE COUNT 380 a 583 c 529 g 375 t

DEFINITION
Sequence 1 from Patent WO0120003.
ACCESSION
AX099774
VERSION
AX099774.1 GI:13538808
KEYWORDS
SOURCE
pig.
ORGANISM
Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 1867)
AUTHORS
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., Le Roy, P. and Chardon, P.

TITLE
Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
JOURNAL
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)

FEATURES
source
Location/Qualifiers
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/organism="Sus scrofa"
/db_xref="taxon:9823"
/note="unnamed protein product"
/codon_start=1
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/db_xref="GI:13538809"
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BASE COUNT 380 a 583 c 529 g 375 t

ORIGIN
Query Match 2.7%; Score 44; DB 6; Length 1867;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
AF214520
LOCUS
DEFINITION
Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
ACCESSION
AF214520
VERSION
AF214520.1 GI:8215683
KEYWORDS
SOURCE
Sus scrofa.

ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 1873)
AUTHORS
Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Raak, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P. and Andersson, L.

TITLE
A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle
JOURNAL
Science 288 (5469), 1248-1251 (2000)
MEDLINE
20280150
PUBMED
10818001
REFERENCE
2 (bases 1 to 1873)
AUTHORS
Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N., Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.

Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,

FEATURES
source
Location/Qualifiers
1..821
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 139 a 219 c 259 g 204 t

Query Match 3.2%; Score 52; DB 6; Length 821;
Best Local Similarity 100.0%; Pred. No. 8.6e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGTCTGGGCTGCCACATGACCGCGGCTGGAGCAGCAGCTGGCGAGG 52

Db 313 TTGGTCTGGGCTGCCACATGACCGCGGCTGGAGCAGCAGCTGGCGAGG 364

RESULT 14
AX099774
LOCUS
DEFINITION
Sequence 1 from Patent WO0120003.
ACCESSION
AX099774
VERSION
AX099774.1 GI:13538808
KEYWORDS
SOURCE
pig.
ORGANISM
Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 1867)
AUTHORS
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., Le Roy, P. and Chardon, P.
TITLE
Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
JOURNAL
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)

FEATURES
source
Location/Qualifiers
1..1867
/organism="Sus scrofa"
/db_xref="taxon:9823"
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BASE COUNT 380 a 583 c 529 g 375 t

DEFINITION
Sequence 1 from Patent WO0120003.
ACCESSION
AX099774
VERSION
AX099774.1 GI:13538808
KEYWORDS
SOURCE
pig.
ORGANISM
Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 1867)
AUTHORS
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., Le Roy, P. and Chardon, P.

TITLE
Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
JOURNAL
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)

FEATURES
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Location/Qualifiers
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BASE COUNT 380 a 583 c 529 g 375 t

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 529 GTCATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGC 572

RESULT 15
AF214520
LOCUS
DEFINITION
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ACCESSION
AF214520
VERSION
AF214520.1 GI:8215683
KEYWORDS
SOURCE
Sus scrofa.

ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 1873)
AUTHORS
Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Raak, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P. and Andersson, L.

TITLE
A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle
JOURNAL
Science 288 (5469), 1248-1251 (2000)
MEDLINE
20280150
PUBMED
10818001
REFERENCE
2 (bases 1 to 1873)
AUTHORS
Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N., Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.

Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,

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Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Job time : 4648.03 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 09:44:41 ; Search time 314.832 Seconds
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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 15

Total number of hits satisfying chosen parameters: 6064

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1372	83.3	2115	22	AAD03320 Human AMPK gamma s
3	1366	82.9	2109	22	AAD03296 Human AMPK gamma s
4	406	24.7	989	22	AAH43682 PRKAG3 intron 2 -
5	398	24.2	547	22	ABA08485 Human AMP-activate
6	278	16.9	1014	22	AAH43684 PRKAG3 intron 10 -
7	252	15.3	3425	22	AAK72740 Human immune/haema
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C	13	85	5.2	378	22	AAK03423	Human brain expres
C	14	85	5.2	378	22	AAK28874	Human bone marrow
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C	20	54	3.3	92	22	ABA49850	Human foetal liver
C	21	54	3.3	92	22	ABA67769	Probe #13292 for g
C	22	54	3.3	92	22	ABA34826	Human brain expres
C	23	54	3.3	92	22	AAK16181	Human bone marrow
C	24	54	3.3	92	22	AAK41922	Probe #12625 for g
C	25	54	3.3	92	22	AAI22692	Probe #16674 used
C	26	54	3.3	92	22	AAI47988	Probe #8345 used t
C	27	54	3.3	92	22	AAI08354	Human genome-deriv
C	28	52	3.2	821	22	AAH43681	PRKAG3 5'untranscr
C	29	44	2.7	1867	22	AAD03295	Pig AMPK gamma sub
C	30	44	2.7	1873	22	AAD03319	Pig AMPK gamma sub
C	31	44	2.7	1873	24	AAD36456	Pig wild-type PRKA
C	32	44	2.7	1873	24	AAD36457	Pig PRKAG3 polymor
C	33	44	2.7	1873	24	AAD36458	Pig PRKAG3 polymor
C	34	44	2.7	1873	24	AAD36459	Pig PRKAG3 polymor
C	35	44	2.7	1873	24	AAD36460	Pig PRKAG3 polymor
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C	41	20	1.2	3385	24	AAD22073	Dermacentor melano
C	42	19	1.2	21	24	AAD36471	Pig PRKAG3 gene co
C	43	19	1.2	22	24	AAD36463	Pig PRKAG3 gene co
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ALIGNMENTS

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XX 21-JAN-2002 (first entry)
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XX PRKAG3 CDNA.
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KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
metabolic disease; diabetes; obesity; substitution; ss.
XX Homo sapiens.
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PN WO200177305-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-SE00765.
XX 07-APR-2000; 2000US-195665P.
XX (AREX-) AREXIS AB.
XX
XX Andersson L, Luthman H, Marklund S;
XX WPI; 2001-657170/75.
XX P-PSDB; QQB47679.
XX
XX New variants of human AMP-activated protein kinase gamma3 subunit
XX associated with a metabolic disease e.g. diabetes or obesity and method
XX for determining a risk estimate of diseases in subject by detecting the
XX variant -
XX
XX Disclosure; Fig 5; 25pp; English.
XX
XX This sequence represents the full length cDNA encoding the human
XX AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting
XX the presence of the PRKAG3 DNA, or a variant, is useful in determining
XX a risk estimate of a metabolic disease, such as diabetes or obesity,
XX in a subject. The variation may occur in exons 3, 4 or 10. In exon
XX 3 variation may be a substitution of a G for a C at nucleotide 320,
XX resulting in the amino acid substitution P71A; in exon 4 variation may
XX be a substitution of a T for a C at nucleotide 550; and in exon 10
XX variation may be a substitution of a T for a C at nucleotide 1037,
XX resulting in the amino acid substitution R340W. There may also be
XX nucleotide variation in intron 6. The numbering of these
XX variations is based on the full length cDNA as given, rather than on
XX position 1 of the open reading frame.
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Best Local Similarity 100.0%; Pred. No. 0;
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Oy 361 GGACTGCTCCCTCTGACTGTACAGCCTCAGCTGAGGCTCCAGCAGATGATGTGGA 420
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Oy 481 AGAGAGCCTGCCCCCTGTGCTGTCCCGCAGGCCCATTTCCCAAGCTGGGCTGGATGA 540
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RESULT 3

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XX AAD03296;
XX AC
XX XX
XX DT 13-JUN-2001 (first entry)
XX XX
DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
XX Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.
OS Homo sapiens.
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XX XX
XX PD 22-MAR-2001.
XX XX
XX PF 11-SEP-2000; 2000WO-EP09896.
XX XX
XX PR 10-SEP-1999; 99EP-0402236.
XX PR 18-MAY-2000; 2000EP-0401388.
XX XX
XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX (ANDE/) ANDERSSON L.

(LOOF/) LOOFT C.
(KALM/) KALM E.
Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
Tannuccelli N, Gellin J, Le Roy P, Chardon P;
XX WPI; 2001-244810/25.
DR P-PSDB; AAE00221.
XX
PT New variants of the gamma subunit of vertebrate adenosine
PT monophosphate-activated kinase for diagnosis or treatment
PT associated with energy metabolism such as diabetes, obesity, and
PT myopathy -
XX
PS Claim 12; Fig 2; 71pp; English.
XX
CC The present sequence is a cDNA encoding human adenosine monophosphate
CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
CC PRKAG3. Mutation in Prkag3 results in an altered regulation of
CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
CC useful as therapeutic for treating carbohydrate metabolism disorders such
CC as diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.
XX
SQ Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;

Query Match 82.9%; Score 1366; DB 22; Length 2109;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 101 TTCTAGAGCAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACAGAGTCTCAGAA 160
Db 1 TTCTAGAGCAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACAGAGTCTCAGAA 60
Oy 161 AGAATCCGTGGAAACCGAGGGCCAAAGCCCTTGAGATGGACAGGAGAGTCCGTGGAG 220
Db 61 AGAATCCGTGGAAACCGAGGGCCAAAGCCCTTGAGATGGACAGGAGAGTCCGTGGAG 120
Oy 221 GAAGGGAGCCACAGGTCAGGGGAAAGGTCCCGGTCCAGGCCAGCTGTGAGTCCACC 280
Db 121 GAAGGGAGCCACAGGTCAGGGGAAAGGTCCCGGTCCAGGCCAGCTGTGAGTCCACC 180
Oy 281 GGGCTGGAGGCCACATTCGCCAAGACACACCCCTTGCTGCTCAAGCTGATCTGCCGGGTG 340
Db 181 GGGCTGGAGGCCACATTCGCCAAGACACACCCCTTGCTGCTCAAGCTGATCTGCCGGGTG 240
Oy 341 GGCACTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTACAGCTCAGCTGCAGGC 400
Db 241 GGCACTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTACAGCTCAGCTGCAGGC 300
Oy 401 TCCAGCAGATGATGTGGAGCTGGCCACGAGTTCCAGCCACAGAGGCTGGAGTGT 460
Db 301 TCCAGCAGATGATGTGGAGCTGGCCACGAGTTCCAGCCACAGAGGCTGGAGTGT 360
Oy 461 GAGCTAGAGGCTGTGGAGAGAGGCTGCTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCT 520
Db 361 GAGCTAGAGGCTGTGGAGAGAGGCTGCTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCT 420
Oy 521 CCNAGCTGGGCTGGGATGACGAACCTCGGAAACCCGGGCCCCAGATCTACATGCGCTTC 580


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PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.

PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0254097.
PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure; SEQ ID NO 27552; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins, and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention.
XX
XX SQ Sequence 3425 BP; 916 A; 794 C; 951 G; 764 T; 0 Other;

Query Match 15.3%; Score 252; DB 22; Length 3425;
Best Local Similarity 100.0%; Pred. No. 5.1e-111;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1396	CGAGACCAGCATCTCTTGGCGTGGTCTCCCTCTCCGACATCCTTACGGCACTGGTGCT	14515
Db	3425	CGAGACCAGCATCTCTTGGCGTGGTCTCCCTCTCCGACATCCTTACGGCACTGGTGCT	3366
Qy	1456	CAGCCCTGCTGGCATGATGCCCTCGGGGCCCTGAGAAGATCTGAGTCTCAATCCCAAGC	1515
Db	3365	CAGCCCTGCTGGCATGATGCCCTCGGGGCCCTGAGAAGATCTGAGTCTCAATCCCAAGC	3306
Qy	1516	CACCTGCACACCTTGGAGGCCAATGAAGGAACTGGAGAACTCAGCCTTTCATCTTCCCCCA	1575
Db	3305	CACCTGCACACCTTGGAGGCCAATGAAGGAACTGGAGAACTCAGCCTTTCATCTTCCCCCA	3246
Qy	1576	CCCCCATTTGCTGGTCAGCTATGATTACGTTAGGTCTGCCCTGGGCCATGACACCAAGC	1635
Db	3245	CCCCCATTTGCTGGTCAGCTATGATTACGTTAGGTCTGCCCTGGGCCATGACACCAAGC	3186
Qy	1636	CTCTTAGTCTTC	1647
Db	3185	CTCTTAGTCTTC	3174
RESULT 8			
AAK72741/c			
ID	AAK72741 standard; DNA; 3425 BP.		
XX	AAK72741;		
AC	AAK72741;		
XX			
DT	06-NOV-2001 (first entry)		
XX			
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27553.		
XX			
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;		
KW	cytostatic; gene therapy; vaccine; metastasis; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200157182-A2.		
XX			
PD	09-AUG-2001.		
XX			
PF	17-JAN-2001; 2001WO-US01354.		
XX			
PR	31-JAN-2000; 2000US-0179065.		
PR	04-FEB-2000; 2000US-0180628.		
PR	24-FEB-2000; 2000US-0184664.		
PR	02-MAR-2000; 2000US-0186350.		
PR	16-MAR-2000; 2000US-0189874.		
PR	17-MAR-2000; 2000US-0190076.		
PR	18-APR-2000; 2000US-0198123.		
PR	19-MAY-2000; 2000US-0205515.		
PR	07-JUN-2000; 2000US-0209467.		
PR	28-JUN-2000; 2000US-0214886.		
PR	30-JUN-2000; 2000US-0215135.		
PR	07-JUL-2000; 2000US-0216647.		
PR	07-JUL-2000; 2000US-0216880.		
PR	11-JUL-2000; 2000US-0217487.		
PR	11-JUL-2000; 2000US-0217496.		
PR	14-JUL-2000; 2000US-0218290.		
PR	26-JUL-2000; 2000US-0220963.		
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PR	14-AUG-2000; 2000US-0224518.		
PR	14-AUG-2000; 2000US-0224519.		
PR	14-AUG-2000; 2000US-0225213.		
PR	14-AUG-2000; 2000US-0225214.		
PR	14-AUG-2000; 2000US-0225266.		
PR	14-AUG-2000; 2000US-0225267.		
PR	14-AUG-2000; 2000US-0225268.		
PR	14-AUG-2000; 2000US-0225270.		
PR	14-AUG-2000; 2000US-0225477.		
PR	14-AUG-2000; 2000US-0225757.		
PR	14-AUG-2000; 2000US-0225758.		
PR	14-AUG-2000; 2000US-0225759.		
PR	18-AUG-2000; 2000US-0226279.		


```
FT XX /note= "5' portion of intron 10"
PN XX
XX WO200177305-A2.
XX
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-SE00765.
XX PF
XX 07-APR-2000; 2000US-195665P.
XX PR
XX (AREX-) AREXIS AB.
XX PA
XX Andersson L, Luthman H, Marklund S;
XX PI
XX WPI; 2001-657170/75.
XX DR
XX New variants of human AMP-activated protein kinase gamma3 subunit
PT associated with a metabolic disease e.g. diabetes or obesity and method
PT for determining a risk estimate of diseases in subject by detecting the
PT variant -
XX
XX Example 1; Fig 3; 25pp; English.
PS
XX The sequences given in AAH43681-84 represents genomic fragments
CC encoding the human AMP-activated protein kinase gamma 3 subunit
CC (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,
CC is useful in determining a risk estimate of a metabolic disease,
CC such as diabetes or obesity, in a subject. The variation may occur
CC in exons 3, 4 or 10. In exon 3 variation may be a substitution of
CC a G for a C at nucleotide 320, resulting in the amino acid
CC substitution P71A; in exon 4 variation may be a substitution of a
CC T for a C at nucleotide 550; and in exon 10 variation may be a
CC substitution of a T for a C at nucleotide 1037, resulting in the
CC amino acid substitution R340W. There may also be nucleotide variation
CC in intron 6.
XX
XX Sequence 1722 BP; 321 A; 504 C; 534 G; 363 T; 0 other;
SQ
Query Match 10.2%; Score 168; DB 22; Length 1722;
Best Local Similarity 100.0%; Pred. No. 1.5e-70;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1022 GGTTCCTGCTGCGCCGCTCTTCTTACCGCACTATCCAGATTTGGGCATCGGC 1081
DB 1523 GGTTCCTGCTGCGCCGCTCTTCTTACCGCACTATCCAGATTTGGGCATCGGC 1502
QY 1082 ACATTCCGAGACTTGGCTGTGGTCTGGAGACAGCACCCATCCTGACTGCATCGACATC 1141
DB 1583 ACATTCCGAGACTTGGCTGTGGTCTGGAGACAGCACCCATCCTGACTGCATCGACATC 1642
QY 1142 TTTGTGACCGCGCTGTGTCTGCACTGCTGTGTTCAACGAATGTGGT 1189
DB 1643 TTTGTGACCGCGCTGTGTCTGCACTGCTGTGTTCAACGAATGTGGT 1690
RESULT 10
ABA44706/c
ID ABA44706 standard; DNA; 378 BP.
XX
XX ABA44706;
AC
XX
DT 01-FEB-2002 (first entry)
XX
DE Human breast cell single exon nucleic acid probe #3401.
XX
XX Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer; ss.
XX
XX Homo sapiens.
OS
XX WO200157271-A2.
PN
XX 09-AUG-2001.
PD
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XX 30-JAN-2001; 2001WO-US00662.
PF
XX 04-FEB-2000; 2000US-0180312.
PR
XX 26-MAY-2000; 2000US-0207456.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.
PR
XX 21-SEP-2000; 2000US-0234687.
PR
XX 27-SEP-2000; 2000US-0236359.
PR
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.
XX
XX New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
XX Claim 1; SEQ ID NO 3401; 327pp + sequence listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and Bt 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence.
CC The present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
SQ
Query Match 5.2%; Score 85; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 651 AGATCAAGAGGCTTCTTTGCTCTGTCGCAACGGTGTGGCGGAGCCCTCTATGGG 710
DB 351 AGATCAAGAGGCTTCTTTGCTCTGTCGCAACGGTGTGGCGGAGCCCTCTATGGG 292
QY 711 ACAGCAAGAGCAGAGCTTTGTGGG 735
DB 291 ACAGCAAGAGCAGAGCTTTGTGGG 267
RESULT 11
ABA55162/c
ID ABA55162 standard; DNA; 378 BP.
XX
XX ABA55162;
AC
XX
DT 01-FEB-2002 (first entry)
XX
XX Human foetal liver single exon nucleic acid probe #3467.
DE
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
KW
XX Homo sapiens.
OS
XX WO200157277-A2.
PN
XX
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PR 09-AUG-2001.
PF 30-JAN-2001; 2001WO-US00669.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver -
XX Claim 1; SEQ ID NO 3467; 639pp + sequence listing; English.
XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX fetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
XX
Query Match 5.2%; Score 85; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 651 AGATCAAGAAGCGCTTCTTCTGTGGGCCAACGGTGCGGGCAGCCCTCTATGGG 710
Db |||||
351 AGATCAAGAAGCGCTTCTTCTGTGGGCCAACGGTGCGGGCAGCCCTCTATGGG 292
QY 711 ACAGCAAGACGACAGCTTTGTGGG 735
Db |||||
291 ACAGCAAGACGACAGCTTTGTGGG 267
RESULT 12
ABA24907/C
ID ABA24907 standard; DNA; 378 BP.
XX
XX ABA24907;
XX
XX 23-JAN-2002 (first entry)
XX
XX Probe #3373 for gene expression analysis in human heart cell sample.
XX Human; gene expression; heart; microarray; vascular system; probe;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; ss.
XX Homo sapiens.
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00666.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX
XX 09-AUG-2001.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488999/53.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX Claim 1; SEQ ID No 3373; 530pp; English.
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
XX
Query Match 5.2%; Score 85; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 651 AGATCAAGAAGCGCTTCTTCTGTGGGCCAACGGTGCGGGCAGCCCTCTATGGG 710
Db |||||
351 AGATCAAGAAGCGCTTCTTCTGTGGGCCAACGGTGCGGGCAGCCCTCTATGGG 292
QY 711 ACAGCAAGACGACAGCTTTGTGGG 735
Db |||||
291 ACAGCAAGACGACAGCTTTGTGGG 267
RESULT 13
AAK03423/C
ID AAK03423 standard; DNA; 378 BP.
XX
XX AAK03423;
XX
XX 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe SEQ ID NO: 3414.
XX Human; brain expressed exon; gene expression analysis; probe;
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX epilepsy; cancer; ss.
XX Homo sapiens.
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00667.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
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XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX PS Example 4; SEQ ID NO: 3414; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system,
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
XX
XX Query Match 5.2%; Score 85; DB 22; Length 378;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-30;
XX Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 651 AGATCAAGAAGCCCTCTTTGCTCTGGTGCCCAACGGTGTGGGGCAGCCCTCTATGGG 710
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
351 AGATCAAGAAGCCCTCTTTGCTCTGGTGCCCAACGGTGTGGGGCAGCCCTCTATGGG 292
Oy 711 ACAGCAAGAAGCAGAGCTTTGTGGG 735
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
291 ACAGCAAGAAGCAGAGCTTTGTGGG 267

RESULT 14
AAK28874/c
ID AAK28874 standard; DNA; 378 BP.
AC AAK28874;
XX
XX 06-NOV-2001 (first entry)
XX Human bone marrow expressed single exon probe SEQ ID NO: 3431.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX Homo sapiens.
XX
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00668.
XX
XX 04-FEB-2000; 2000US-0180312.
XX
XX 26-MAY-2000; 2000US-0207456.
XX
XX 30-JUN-2000; 2000US-0608408.
XX
XX 03-AUG-2000; 2000US-0632366.
XX
XX 21-SEP-2000; 2000US-0234687.
XX
XX 27-SEP-2000; 2000US-0236359.
XX
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow -
```

```
PS Example 4; SEQ ID NO: 3431; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX the probes of the invention.
XX SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
XX
XX Query Match 5.2%; Score 85; DB 22; Length 378;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-30;
XX Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 651 AGATCAAGAAGCCCTCTTTGCTCTGGTGCCCAACGGTGTGGGGCAGCCCTCTATGGG 710
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
351 AGATCAAGAAGCCCTCTTTGCTCTGGTGCCCAACGGTGTGGGGCAGCCCTCTATGGG 292
Oy 711 ACAGCAAGAAGCAGAGCTTTGTGGG 735
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
291 ACAGCAAGAAGCAGAGCTTTGTGGG 267

RESULT 15
AAI13465/c
ID AAI13465 standard; DNA; 378 BP.
XX
XX AAI13465;
XX
XX 12-OCT-2001 (first entry)
XX
XX Probe #3398 for gene expression analysis in human cervical cell sample.
XX
XX Probe; human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200157278-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00670.
XX
XX 04-FEB-2000; 2000US-0180312.
XX
XX 26-MAY-2000; 2000US-0207456.
XX
XX 30-JUN-2000; 2000US-0608408.
XX
XX 03-AUG-2000; 2000US-0632366.
XX
XX 21-SEP-2000; 2000US-0234687.
XX
XX 27-SEP-2000; 2000US-0236359.
XX
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human cervical epithelial cells -
XX
XX Claim 25; SEQ ID No 3398; 487pp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
XX (SENP). The present sequence is one such probe. The SENPs are derived
XX from human HeLa cells. The SENPs can be used to produce a single exon
XX microarray, which can be used for measuring human gene expression in a
XX sample derived from human cervical epithelial cells. By measuring gene
XX expression, the probes are therefore useful in grading and/or staging
XX of diseases of the cervix, notably cervical cancer.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
```

```
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match      5.2%; Score 85; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 651 AGATCAAGAGCCCTTCTTTGCTCTGGTGGCCAAAGGTGTGGGGCAGCCCTCTATGGG 710
DB 351 AGATCAAGAGCCCTTCTTTGCTCTGGTGGCCAAAGGTGTGGGGCAGCCCTCTATGGG 292

QY 711 ACAGCAAGAGCAGAGCTTTGTGGG 735
DB 291 ACAGCAAGAGCAGAGCTTTGTGGG 267
```

```
Search completed: January 6, 2003, 09:56:02
Job time : 329.832 secs
```

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 09:44:42 ; Search time 2107.51 Seconds
(without alignments)
12656.598 Million cell updates/sec

Title: US-09-826-581-5
Perfect score: 1647
Sequence: 1 ttgctctgggctggccaca.....acaccagcctcttagtcttc 1647

Scoring table: OLIGO_NUC
Gapex 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 15

Total number of hits satisfying chosen parameters: 44986

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estlin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estcom:*
 - 17: gb_gss:*
 - 18: em_gss_hum:*
 - 19: em_gss_inv:*
 - 20: em_gss_pln:*
 - 21: em_gss_vrt:*
 - 22: em_gss_fun:*
 - 23: em_gss_man:*
 - 24: em_gss_mus:*
 - 25: em_gss_other:*
 - 26: em_gss_pro:*
 - 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	10.0	413	9	AA178898
2	68	4.1	485	14	W94830
3	42	2.6	572	13	B1344527
4	41	2.5	399	10	AW356079
5	41	2.5	422	10	AW427435
6	41	2.5	444	12	BF890374

7	41	2.5	548	13	BI775360
8	37	2.2	298	10	AW314499
9	24	1.5	461	10	BE126712
10	24	1.5	595	13	BM487789
11	24	1.5	636	12	BG713637
12	24	1.5	687	9	AJ451523
13	24	1.5	758	9	AJ396118
14	23	1.4	474	12	BF601364
15	22	1.3	124	13	BI012981
16	22	1.3	372	13	BM490188
17	22	1.3	563	13	BI555697
18	21	1.3	286	10	BB527609
19	21	1.3	356	10	AW124415
20	21	1.3	356	12	BF456027
21	21	1.3	357	13	BI134322
22	21	1.3	504	12	BF710369
23	21	1.3	518	12	BF999510
24	21	1.3	538	17	AQ431286
25	21	1.3	609	10	BB634609
26	21	1.3	621	10	BB628877
27	21	1.3	655	10	BB629521
28	21	1.3	685	10	BB630381
29	21	1.3	686	17	BH460875
30	21	1.3	697	17	AZ942448
31	21	1.3	933	13	BI662109
32	21	1.3	954	17	AZ690459
33	20	1.2	132	13	BI013023
34	20	1.2	157	10	AV321038
35	20	1.2	222	13	BG997440
36	20	1.2	291	17	AZ745562
37	20	1.2	500	9	AL780430
38	20	1.2	533	9	AI477537
39	20	1.2	548	17	AQ693634
40	20	1.2	549	9	AA562894
41	20	1.2	589	13	BI766104
42	20	1.2	621	9	AA167839
43	20	1.2	660	17	AZ360277
44	20	1.2	789	13	BI871153
45	20	1.2	851	9	AL519471

ALIGNMENTS

RESULT 1
AA178898
LOCUS
DEFINITION
z38d10.r1 Stratagene muscle 937209 Homo sapiens CDNA clone
IMAGE:611731.5' similar to SW:AAKG_RAT P80385 5'-AMP-ACTIVATED
PROTEIN KINASE, GAMMA CHAIN ;, mRNA sequence.
ACCESSION
AA178898
VERSION
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 413)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
TITLE
JOURNAL
COMMENT
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1280 Std Error: 0.00

AA178898 413 bp mRNA linear EST 09-MAR-1998
z38d10.r1 Stratagene muscle 937209 Homo sapiens CDNA clone
IMAGE:611731.5' similar to SW:AAKG_RAT P80385 5'-AMP-ACTIVATED
PROTEIN KINASE, GAMMA CHAIN ;, mRNA sequence.

Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 255.

FEATURES

Location/Qualifiers
1. .413
/organism="Homo sapiens"
/db_xref="GDB:4643570"
/db_xref="taxon:9606"
/clone="IMAGE:611731"
/clone_lib="Stratagene muscle 937209"
/tissue_type="muscle"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skeletal muscle; Vector: pBluescript SK-;
Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally.
Primer: Oligo dt. Skeletal muscle from patient with
malignant hyperthermia. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGAG
3' ~3' adaptor sequence: 5' CTCAGTTTTTTTTTTTTTTT 3"

BASE COUNT

80 a 109 c 117 g 102 t 5 others

ORIGIN

Query Match 10.0%; Score 164; DB 9; Length 413;
Best Local Similarity 100.0%; Pred. No. 4.9e-65;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1121 ATCTGACTGCTGACATCTTTGTGGACCGCGTGTCTGCACTGCTGGTCAAC 1180
|||||
Db 79 ATCTGACTGCTGACATCTTTGTGGACCGCGTGTCTGCACTGCTGGTCAAC 138
|||||
QY 1181 GAATGTGTCAGTCTGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCCAG 1240
|||||
Db 139 GAATGTGTCAGTCTGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCCAG 198
|||||
QY 1241 CAAACCTACAACTGCTGACATGCTGGGAGAGCCCTGAG 1284
|||||
Db 199 CAAACCTACAACTGCTGACATGCTGGGAGAGCCCTGAG 242
|||||

RESULT 2

W94830
LOCUS 485 bp mRNA linear EST 29-NOV-1996
DEFINITION zell3e0.r1 Soares fetal_heart_NbHH19W Homo sapiens cDNA clone
IMAGE:35890 5', mRNA sequence.
W94830
ACCESSION W94830.1 GI:1423951
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 485)
Hillier, L., Clark, N., Dubucque, T., Elliston, K., Hawkins, M., Holman
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston
R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

TITLE

JOURNAL

COMMENT

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 775 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 431.

FEATURES

Location/Qualifiers
1. .485
/organism="Homo sapiens"
/db_xref="GDB:1275434"
/db_xref="taxon:9606"

source

/clone="IMAGE:35890"
/clone_lib="Soares fetal_heart_NbHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: p7713D (pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7713 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."

BASE COUNT 91 a 161 c 119 g 112 t 2 others

Query Match 4.1%; Score 68; DB 14; Length 485;
Best Local Similarity 99.2%; Pred. No. 1.9e-20;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1488 GAGAGATCTGAGTCTCAATCCCAAGCCACCTGCACACCTGGAGGCCAATGAAGGGAAAC 1547
|||||
Db 65 GAGAGATCTGAGTCTCAATCCCAAGCCACCTGCACACCTGGAGGCCAATGAAGGGAAAC 124
|||||
QY 1548 TGGAGAACTGAGCTTCATCTTCCCAACCCCATTTGCTGTTTCAGTATGATTCAGG 1606
|||||
Db 125 TGGAGAACTGAGCTTCATCTTCCCAACCCCATTTGCTGTTTCAGTATGATTCAGG 183
|||||

RESULT 3

BI344527
LOCUS 572 bp mRNA linear EST 30-JUL-2001
DEFINITION 373008 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BI344527
VERSION BI344527.1 GI:15037807
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 572)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68913-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers

JOURNAL

COMMENT

FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCAGTCACGACG
Plate: 119 row: I column: 11
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
1. .572
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;

FEATURES

source
Location/Qualifiers
1. .572
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;

Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 106 a 190 c 151 g 124 t 1 others

ORIGIN

Query Match 2.6%; Score 42; DB 13; Length 572;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1247 TACACACCTGGACATGAGTGTGGAGAGCCCTGAGGCAG 1288
|||||
Db 409 TACAACACCTGGACATGAGTGTGGAGAGCCCTGAGGCAG 450
|||||

RESULT 4
AW356079

LOCUS 399 bp mRNA linear EST 25-APR-2001

DEFINITION 38073 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION AW356079

VERSION AW356079.1 GI:6860085

KEYWORDS EST.

SOURCE cow.

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 399)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett ,G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)

MEDLINE 21180013

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCCGACGACGACG
Plate: 17 row: P column: 9
Seq primer: ATTTAGGTGACACTATAG.

FEATURES source
1..399
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
100 a 126 c 117 g 56 t

BASE COUNT 100 a 126 c 117 g 56 t

ORIGIN

Query Match 2.5%; Score 41; DB 10; Length 399;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 CAGCTGCTGAGTCCACCGGCTGGAGGCCACATTTCCCAAG 304
|||||
Db 206 CAGCTGCTGAGTCCACCGGCTGGAGGCCACATTTCCCAAG 246
|||||

RESULT 5
AW427435

LOCUS 422 bp mRNA linear EST 25-APR-2001

DEFINITION 63185 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION AW427435

VERSION AW427435.1 GI:6955382

KEYWORDS EST.

SOURCE cow.

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 422)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett ,G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)

MEDLINE 21180013

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCCGACGACGACG
Plate: 32 row: F column: 22
Seq primer: ATTTAGGTGACACTATAG.

FEATURES source
1..422
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."
102 a 136 c 125 g 59 t

BASE COUNT 102 a 136 c 125 g 59 t

ORIGIN

Query Match 2.5%; Score 41; DB 10; Length 422;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 CAGCTGCTGAGTCCACCGGCTGGAGGCCACATTTCCCAAG 304
|||||
Db 254 CAGCTGCTGAGTCCACCGGCTGGAGGCCACATTTCCCAAG 294
|||||

RESULT 6
BF890374

LOCUS 444 bp mRNA linear EST 25-APR-2001

DEFINITION 291826 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BF890374

VERSION BF890374.1 GI:12281760

KEYWORDS EST.

SOURCE cow.

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 444)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,

Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W., Rohrer, G.A., Chitko-McKown, C.G., Perteau, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTTCCAGTCACGACG

Plate: 57 row: H column: 11

Seq primer: ATTTAGTGACACTATAG.

FEATURES

source

1..444

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;

Library made from pooled tissue from marrow, alveolar

macrophage, ovary, fetal semitendinosus muscle, and fetal

longissimus muscle."

91 a 147 c 139 g 67 t

BASE COUNT

ORIGIN

Query Match 2.5%; Score 41; DB 12; Length 444;

Best Local Similarity 100.0%; Pred. No. 6.5e-08;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTCCCAAG 304

|||||

DB 59 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTCCCAAG 99

RESULT 7

B1775360

LOCUS

B1775360 548 bp mRNA linear EST 25-SEP-2001

DEFINITION 467815 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION B1775360

VERSION B1775360.1 GI:15776346

KEYWORDS EST.

SOURCE COW.

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 548)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett

, G.L., Heaton, M.P., Laegreid, W., Rohrer, G.A., Chitko-McKown, C.G.,

Perteau, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and

Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTTCCAGTCACGACG

Plate: 90 row: I column: 16

Seq primer: ATTTAGTGACACTATAG.

FEATURES

source

1..548

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 2BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;

Library made from pooled tissue from testis, thymus,

semitendinosus muscle, longissimus muscle, pancreas,

adrenal, and endometrium."

119 a 173 c 163 g 93 t

BASE COUNT

ORIGIN

Query Match 2.5%; Score 41; DB 13; Length 548;

Best Local Similarity 100.0%; Pred. No. 6.8e-08;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTCCCAAG 304

|||||

DB 101 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTCCCAAG 141

RESULT 8

AW314499

LOCUS

AW314499 298 bp mRNA linear EST 25-APR-2001

DEFINITION 10669 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION AW314499

VERSION AW314499.1 GI:6743764

KEYWORDS EST.

SOURCE COW.

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 298)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett

, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,

Perteau, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and

Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 20

and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTTCCAGTCACGACG

Plate: 11 row: H column: 23

Seq primer: ATTTAGTGACACTATAG.

Location/Qualifiers

1..298

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"

/tissue_type="pooled"

BASE COUNT		55 a	96 c	81 g	66 t
ORIGIN					
Query Match					
Best Local Similarity 2.2%; Score 37; DB 10; Length 298;					
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
/lab_host="DH10B"					
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;					
Library made from pooled tissue from marrow, alveolar					
macrophage, ovary, fetal semitendinosus muscle, and fetal					
longissimus muscle."					
Qy	1298	TGTCGGAGGAGTCTTCTCTGCCAGCCCCACGAGA	1334		
Db	227	TGTCGGAGGAGTCTTCTCTGCCAGCCCCACGAGA	263		
RESULT 9					
BE126712 461 bp mRNA linear EST 15-JUN-2000					
LOCUS					
DEFINITION					
DEPA0460 Rat Lambda ZAP Express Library Rattus norvegicus cDNA 5',					
mRNA sequence.					
ACCESSION					
BE126712					
VERSION					
BE126712.1 GI:8549403					
KEYWORDS					
EST.					
SOURCE					
Norway rat.					
ORGANISM					
Rattus norvegicus					
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;					
Rattus.					
REFERENCE					
1 (bases 1 to 461)					
Sleeman,M.A., Murison,J.G., Strachan,L., Kumble,K.D., Glenn,M.P.,					
McGrath,A., Grierson,A., Havukkala,I., Tan,P.L.J. and Watson,J.D.					
Expressed sequence tags of cDNA clones from rat dermal papilla					
cells					
JOURNAL					
Unpublished (2000)					
COMMENT					
Contact: Sleeman MA					
Biology					
Genesis Research and Development Corporation Limited					
P.O. Box 50, 1 Fox St, Parnell, Auckland, New Zealand					
Tel: 0064 9 373 5600					
Fax: 0064 9 373 2189					
Email: m.sleeman@genesis.co.nz					
Seq primer: T3 forward					
High quality sequence stop: 461.					
Location/Qualifiers					
1..461					
/organism="Rattus norvegicus"					
/strain="Dark-Agouti"					
/db_xref="taxon:10116"					
/clone_lib="Rat Lambda ZAP Express Library"					
/tissue_type="vibrissae"					
/cell_type="dermal papilla"					
BASE COUNT					
117 a 114 c 109 g 121 t					
ORIGIN					
Query Match					
Best Local Similarity 1.5%; Score 24; DB 10; Length 461;					
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
/lab_host="DH10B"					
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;					
Library made from pooled tissue from marrow, alveolar					
macrophage, ovary, fetal semitendinosus muscle, and fetal					
longissimus muscle."					
Qy	737	ATGCTGACCATCACTGACTTCATC	760		
Db	246	ATGCTGACCATCACTGACTTCATC	269		
RESULT 10					
BM487789					
LOCUS					
DEFINITION					
pgm2n.pk005.j24 Normalized Chicken Breast Muscle, Leg Muscle, and					
Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA					
clone pgm2n.pk005.j24 5' similar to gb AAC52580.1 (U42413)					
5'-AMP-activated protein kinase, gamma-1 subunit (Rattus norvegicus					
), mRNA sequence.					

```

COMMENT      Contact: Joan Burnside
              Molecular Endocrinology
              University of Delaware
              40 Townsend Hall, Newark, DE 19717, USA
              Tel: 302 831-1345
              Fax: 302-831-3411
              Email: joan@udel.edu, www.chickest.udel.edu.

FEATURES     source
              1. 636
              /organism="Gallus gallus"
              /db_xref="taxon:9031"
              /clone="pglin.pk008.c13"
              /clone_lib="Normalized Liver Library"
              /sex="Male and Female"
              /tissue_type="liver"
              /lab_host="E.coli EMDH10B"
              /note="Vector: pCMVSPORT 6"

BASE COUNT   129 a 215 c 167 g 119 t 6 others
ORIGIN

      Query Match      1.5%; Score 24; DB 12; Length 636;
      Best Local Similarity 100.0%; Pred. No. 5.5;
      Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 737 ATGCTGACCATCACTGACTTCATC 760
      |||||||||||||||||||
Db 286 ATGCTGACCATCACTGACTTCATC 309

RESULT 12
AJ451523      687 bp mRNA linear EST 22-APR-2002
LOCUS      AJ451523 riken1 Gallus gallus cDNA clone 29a6r1, mRNA sequence.
DEFINITION
ACCESSION   AJ451523
VERSION     AJ451523.1 GI:20261619
KEYWORDS    EST.
SOURCE      chicken.
ORGANISM    Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            1 (bases 1 to 687)
            /organism="Gallus gallus"
            /db_xref="taxon:9031"
            /clone="29a6r1"
            /clone_lib="riken1"
            /cell_type="bursal lymphocyte"
            /dev_stage="2-3 weeks old"
            /note="CB inbred strain"

REFERENCE    Buerstedde, J.M.
              Gallus gallus bursal lymphocyte EST
              Unpublished (2002)
              Contact: Buerstedde JM
              Cellular Immunology
              Heinrich-Pette-Institute
              Martinistr. 52, 20251 Hamburg, Germany
              Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES     source
              1. 687
              /organism="Gallus gallus"
              /db_xref="taxon:9031"
              /clone="29a6r1"
              /clone_lib="riken1"
              /cell_type="bursal lymphocyte"
              /dev_stage="2-3 weeks old"
              /note="CB inbred strain"

BASE COUNT   143 a 228 c 191 g 125 t
ORIGIN

      Query Match      1.5%; Score 24; DB 9; Length 687;
      Best Local Similarity 100.0%; Pred. No. 5.6;
      Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 737 ATGCTGACCATCACTGACTTCATC 760
      |||||||||||||||||||
Db 305 ATGCTGACCATCACTGACTTCATC 328

RESULT 13
AJ396118      758 bp mRNA linear EST 25-JAN-2001
LOCUS      AJ396118 dkfz426 Gallus gallus cDNA clone 25f16r1, mRNA sequence.
DEFINITION
ACCESSION   AJ396118
VERSION     AJ396118.1 GI:7127728
KEYWORDS    EST.
SOURCE      chicken.
ORGANISM    Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            1 (bases 1 to 758)
            /organism="Gallus gallus"
            /db_xref="taxon:9031"
            /clone="25f16r1"
            /clone_lib="dkfz426"
            /tissue_type="Bursa of Fabricius"
            /cell_type="bursal lymphocyte"
            /dev_stage="2-3 weeks old"

REFERENCE    J., Korn, B. and Buerstedde, J.M.
              A large database of chicken bursal ESTs as a resource for the
              analysis of vertebrate gene function
              Genome Res. 10 (12), 2062-2069 (2000)
              20568495
              Contact: Buerstedde JM
              Cellular Immunology
              Heinrich-Pette-Institute
              Martinistr. 52, 20251 Hamburg, Germany
              Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES     source
              1. 758
              /organism="Gallus gallus"
              /strain="CB"
              /db_xref="taxon:9031"
              /clone="25f16r1"
              /clone_lib="dkfz426"
              /tissue_type="Bursa of Fabricius"
              /cell_type="bursal lymphocyte"
              /dev_stage="2-3 weeks old"

BASE COUNT   168 a 238 c 186 g 166 t
ORIGIN

      Query Match      1.5%; Score 24; DB 9; Length 758;
      Best Local Similarity 100.0%; Pred. No. 5.8;
      Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 737 ATGCTGACCATCACTGACTTCATC 760
      |||||||||||||||||||
Db 124 ATGCTGACCATCACTGACTTCATC 147

RESULT 14
BF601364      474 bp mRNA linear EST 25-APR-2001
LOCUS      BF601364 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION
ACCESSION   BF601364
VERSION     BF601364.1 GI:11698586
KEYWORDS    EST.
SOURCE      cow.
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
            1 (bases 1 to 474)
            /organism="Bos taurus"
            /db_xref="taxon:9031"
            /clone="MARC 3BOV"
            /cell_type="bursal lymphocyte"
            /dev_stage="2-3 weeks old"

REFERENCE    Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
              Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
              , G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
              Perlea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
              Keefe, J.W.
              Sequence evaluation of four pooled-tissue normalized bovine cDNA
              libraries and construction of a gene index for cattle
              Genome Res. 11 (4), 626-630 (2001)
              21180013
              Contact: Smith TPL
              USDA, ARS, US Meat Animal Research Center
              PO Box 166, Clay Center, NE 68913-0166, USA
              Tel: 402 762 4366
              Fax: 402 762 4390
              Email: smith@email.marc.usda.gov
              Single pass sequencing. Bases called and alt_trimmed with phred

```


v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCAGCAGC

Plate: 40 row: O column: 13

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

1. .474

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site.1: NotI; Site.2: SalI;

Library made from pooled tissue from marrow, alveolar

macrophage, ovary, fetal semitendinosus muscle, and fetal

longissimus muscle."

longissimus muscle."

81 a 173 c 119 g 101 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 1.4%; Score 23; DB 12; Length 474;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1451 GTGCTCAGCCCTGTCGCATCGA 1473

|||||

Db 118 GTGCTCAGCCCTGTCGCATCGA 140

|||||

RESULT 15

BI012981/c

LOCUS

BI012981 124 bp mRNA linear EST 13-JUN-2001

DEFINITION

PM2-ET0206-160101-001-f08 ET0206 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BI012981

VERSION

BI012981.1 GI:14417052

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 124)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-ET0206-

160101-001-f08&t3=2001-01-16&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 16

High quality sequence stop: 124.

Location/Qualifiers

1. .124

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="ET0206"

/dev_stage="Adult"

FEATURES

source

/note="Organ: lung tumor; Vector: puc18; Site.1: SmaI;
Site.2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 30 a 26 c 43 g 25 t

ORIGIN

Query Match

Best Local Similarity 1.3%; Score 22; DB 13; Length 124;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1422 TCTCCCTCTCCGACATCCTTCA 1443

|||||

Db 107 TCTCCCTCTCCGACATCCTTCA 86

|||||

Search completed: January 6, 2003, 11:08:01

Job time : 2115.51 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 09:44:41 ; Search time 329.168 Seconds
(without alignments)
11781.028 Million cell updates/sec

Title: US-09-826-581-3

Perfect score: 1722

Sequence: 1 cctggccctcagatcaaga.....gatgagagctcggctgga 1722

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 15

Total number of hits satisfying chosen parameters: 7349

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002.*

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1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
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4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
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8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
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22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1722	100.0	1722	22	AAH43683
2	346	20.1	378	22	ABA44706
3	346	20.1	378	22	ABA55162
4	346	20.1	378	22	ABA24907
5	346	20.1	378	22	AAK03423
6	346	20.1	378	22	AAK28874
7	346	20.1	378	22	AAI13465
8	346	20.1	378	22	AAI34821
9	346	20.1	378	22	AAI03344

c	10	346	20.1	378	24	ABS03407	Human genome-deriv
	11	168	9.8	1647	22	AAH43685	PRKAG3 cDNA. Homo
	12	168	9.8	2109	22	AAH03296	Human AMPK gamma 8
	13	168	9.8	2115	22	AAH03320	Human AMPK gamma 8
	14	147	8.5	547	22	ABA08485	Human AMP-activate
	15	65	3.8	92	22	ABA49850	Human breast cell
	16	65	3.8	92	22	ABA67769	Human foetal liver
	17	65	3.8	92	22	ABA49826	Probe #13292 for g
	18	65	3.8	92	22	AAK16181	Human brain expres
	19	65	3.8	92	22	AAK41922	Human bone marrow
	20	65	3.8	92	22	AAI26292	Probe #12625 for g
	21	65	3.8	92	22	AAI47988	Probe #16674 used
	22	65	3.8	92	22	AAI08354	Probe #8345 used t
	23	65	3.8	92	22	ABS15953	Human genome-deriv
	24	38	2.2	1867	22	AAH03295	Pig AMPK gamma sub
	25	38	2.2	1873	22	AAH03319	Pig AMPK gamma sub
	26	38	2.2	1873	24	AAH36456	Pig wild-type PRKA
	27	38	2.2	1873	24	AAH36457	Pig PRKAG3 polymor
	28	38	2.2	1873	24	AAH36458	Pig PRKAG3 polymor
	29	38	2.2	1873	24	AAH36459	Pig PRKAG3 polymor
	30	38	2.2	1873	24	AAH36460	Pig PRKAG3 polymor
	31	38	2.2	2022	22	AAH03321	Sus scrofa PRKAG3
	32	24	1.4	5946	13	AAQ28398	Rat nestin gene.
	33	24	1.4	11236	15	AAQ70447	Rat nestin gene.
	34	23	1.3	23	22	AAH43695	PRKAG3 reverse pri
	35	21	1.2	234	24	ABN18013	Human ORFX polynuc
	36	21	1.2	525	22	AAH10581	Human cDNA clone (
	37	19	1.1	23	24	AAH36468	Pig PRKAG3 gene co
	38	19	1.1	190	22	ABA69740	Human foetal liver
	39	19	1.1	190	22	AAK17931	Human brain expres
	40	19	1.1	190	22	AAK43806	Human bone marrow
	41	19	1.1	190	22	AAI49825	Probe #18511 used
	42	19	1.1	190	24	ABS18034	Human genome-deriv
	43	19	1.1	266	21	AAC28698	Human secreted pro
	44	19	1.1	422	21	AAZ65087	Membrane-bound pro
	45	19	1.1	422	22	AAH46045	Human DNA encoding

ALIGNMENTS

RESULT 1

AAH43683
ID AAH43683 standard; DNA; 1722 BP.
AC AAH43683;
XX
DT 21-JAN-2002 (first entry)
XX
DE PRKAG3 intron 4 - intron 10.
XX
KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
metabolic disease; diabetes; obesity; substitution; ds.
XX Homo sapiens.

Key	Location/Qualifiers
intron	1..13
FT	/*tag= a
FT	/number= "Intron 4"
FT	/note= "3', portion of intron 4"
FT	14..95
FT	/*tag= b
FT	/number= "Exon 5"
FT	96..552
FT	/*tag= c
FT	/number= "Intron 5"
FT	553..611
FT	/*tag= d
FT	/number= "Exon 6"
FT	612..736
FT	/*tag= e
FT	/number= "Intron 6"

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FT exon 737..782
FT /*tag= f
FT /number= "Exon 7"
FT intron 783..986
FT /*tag= g
FT /number= "Intron 7"
FT exon 987..1041
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FT /number= "Exon 8"
FT intron 1042..1242
FT /*tag= i
FT /number= "Intron 8"
FT exon 1243..1369
FT /*tag= j
FT /number= "Exon 9"
FT intron 1370..1522
FT /*tag= k
FT /number= "Intron 9"
FT exon 1523..1688
FT /*tag= l
FT /number= "Exon 10"
FT intron 1689..1722
FT /*tag= i
FT /number= "Intron 10"
FT /note= "5' portion of intron 10"
XX WO200177305-A2.
PN
XX
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-SE00765.
XX
XX PR 07-APR-2000; 2000US-195665P.
XX
XX PA (AREX-) AREXIS AB.
XX
XX PI Andersson L, Luthman H, Marklund S;
XX
XX DR WPI; 2001-657170/75.
XX
XX PT New variants of human AMP-activated protein kinase gamma3 subunit
XX associated with a metabolic disease e.g. diabetes or obesity and method
XX for determining a risk estimate of diseases in subject by detecting the
XX variant -
XX
XX PS Example 1; Fig 3; 25pp; English.
XX
XX CC The sequences given in AAH43681-84 represents genomic fragments
XX encoding the human AMP-activated protein kinase gamma 3 subunit
XX (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,
XX is useful in determining a risk estimate of a metabolic disease,
XX such as diabetes or obesity, in a subject. The variation may occur
XX in exons 3, 4 or 10. In exon 3 variation may be a substitution of
XX a G for a C at nucleotide 320, resulting in the amino acid
XX substitution P1A; in exon 4 variation may be a substitution of a
XX T for a C at nucleotide 550; and in exon 10 variation may be a
XX CC substitution of a T for a C at nucleotide 1037, resulting in the
XX CC amino acid substitution R340W. There may also be nucleotide variation
XX in intron 6.
XX
XX SQ Sequence 1722 BP; 321 A; 504 C; 534 G; 363 T; 0 other;

Query Match 100.0%; Score 1722; DB 22; Length 1722;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGCCCCCTCAGATCAAGAGGCGCTTCTTGCTCTGGTGCCCAACGGTGTGGGGCAGC 60
DB 1 CCTGGCCCCCTCAGATCAAGAGGCGCTTCTTGCTCTGGTGCCCAACGGTGTGGGGCAGC 60

QY 61 CCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGTGAGGAGGCTGGGAGGTGAAG 120
DB 61 CCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGTGAGGAGGCTGGGAGGTGAAG 120

```

OY 1201 CTCCTAGGCTGCCCGAGGCTCACTGCTCCCATCTCTGCAGCCTGTTGAAGCTGTCTA 1260
Db |||||
OY 1201 CTCCTAGGCTGCCCGAGGCTCACTGCTCCCATCTCTGCAGCCTGTTGAAGCTGTCTA 1260
Db |||||
OY 1261 CACCTCATCAAGAACCGGATCCATCGCTGCTGTTCTTTGACCCGGTGTCAAGCAAGT 1320
Db |||||
OY 1261 CACCTCATCAAGAACCGGATCCATCGCTGCTGTTCTTTGACCCGGTGTCAAGCAAGT 1320
Db |||||
OY 1321 ACTCCATCTTACACACAAACCGCTGCTCAAGTCTCTGACATCTTTTGAAGCCTGGG 1380
Db |||||
OY 1321 ACTCCATCTTACACACAAACCGCTGCTCAAGTCTCTGACATCTTTTGAAGCCTGGG 1380
Db |||||
OY 1381 CCCAGTGGGAGGAAGGGGAGACCTGGGAGGTGATCAGAGGSCCTGAGGACTCTTCAG 1440
Db |||||
OY 1381 CCCAGTGGGAGGAAGGGGAGACCTGGGAGGTGATCAGAGGSCCTGAGGACTCTTCAG 1440
Db |||||
OY 1441 CCTAGCAGTCTGGGGAAGAGCTGGGAGCCCTCTTTGAAGCTCTGGATCCCTGATCTCC 1500
Db |||||
OY 1441 CCTAGCAGTCTGGGGAAGAGCTGGGAGCCCTCTTTGAAGCTCTGGATCCCTGATCTCC 1500
Db |||||
OY 1501 ACCTGTCTCCATCTTAACCAAGGTTCCCTGCTGCTGCCCGCCCTCTCTCTACCGCAC 1560
Db |||||
OY 1501 ACCTGTCTCCATCTTAACCAAGGTTCCCTGCTGCTGCCCGCCCTCTCTCTACCGCAC 1560
Db |||||
OY 1561 TATCCAAGATTTGGGCATCGGCACATTTCCGAGACTTTGGCTGTGGTCTGGAGACAGCAC 1620
Db |||||
OY 1561 TATCCAAGATTTGGGCATCGGCACATTTCCGAGACTTTGGCTGTGGTCTGGAGACAGCAC 1620
Db |||||
OY 1621 CATCTGACTGCACTGGACATCTTTTGTGACCGCGGTGTGTCTGCACTGCCTGTGGTCAA 1680
Db |||||
OY 1621 CATCTGACTGCACTGGACATCTTTTGTGACCGCGGTGTGTCTGCACTGCCTGTGGTCAA 1680
Db |||||
OY 1681 CGAATGTGTGTACCCACCCAGGATGAGAGGCTCGGGCTGGA 1722
Db |||||
OY 1681 CGAATGTGTGTACCCACCCAGGATGAGAGGCTCGGGCTGGA 1722
Db |||||

RESULT 2

ABA44706/c
ID ABA44706 standard; DNA; 378 BP.

XX AC

XX AC

XX AC

XX 01-FEB-2002 (first entry)

XX Human breast cell single exon nucleic acid probe #3401.

XX Human; microarray; single exon probe; gene expression; breast;

XX disease; cancer; ss.

XX Homo sapiens.

XX WO200157271-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00662.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes,

XX PT

PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
PS Claim 1; SEQ ID NO 3401; 327pp + sequence listing; English.

XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match 20.1%; Score 346; DB 22; Length 378;

Best Local Similarity 100.0%; Pred. No. 1.6e-148;

Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTGCCCCCTCAGATCAAGAAGGCTTCTTTGCTCTGCTGCCCCAACGGTGTCCGGCAGC 60

Db |||||

OY 362 COTGGCCCCCTCAGATCAAGAAGGCTTCTTTGCTCTGCTGCCCCAACGGTGTCCGGCAGC 303

Db |||||

OY 61 CCTCTATGGGACAGCAAGAGAGCTTTGTGGTTCAGGAGAGGCTGGGGAGGTGAAG 120

Db |||||

OY 302 CCTCTATGGGACAGCAAGAGAGCTTTGTGGTTCAGGAGAGGCTGGGGAGGTGAAG 243

Db |||||

OY 121 GGAGATGAGGAGGTGAGGGGAGATCTTGATCGTGTGTTCTGGGGCTGATCTCTGATAT 180

Db |||||

OY 242 GGAGATGAGGAGGTGAGGGGAGATCTTGATCGTGTGTTCTGGGGCTGATCTCTGATAT 183

Db |||||

OY 181 ACCACAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCGAGGGTGGAGAAAGTCCATCC 240

Db |||||

OY 182 ACCACAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCGAGGGTGGAGAAAGTCCATCC 123

Db |||||

OY 241 GGAGTCTGCATGGCCAGCTGGGAGACCTCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300

Db |||||

OY 122 GGAGTCTGCATGGCCAGCTGGGAGACCTCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63

Db |||||

OY 301 ATGACAGCTGACACCTTTTCACTCCGCTACTGCATGCCCCCTGTGC 346

Db |||||

OY 62 ATGACAGCTGACACCTTTTCACTCCGCTACTGCATGCCCCCTGTGC 17

Db |||||

RESULT 3

ABA55162/c

ID ABA55162 standard; DNA; 378 BP.

XX AC

XX AC

XX AC

XX ABA55162;

XX 01-FEB-2002 (first entry)

XX Human foetal liver single exon nucleic acid probe #3467.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 09-AUG-2001.

XX 09-AUG-2001.

XX 09-AUG-2001.

XX 09-AUG-2001.

XX 09-AUG-2001.

XX 09-AUG-2001.

XX 09-AUG-2001.

XX 09-AUG-2001.

XX 09-AUG-2001.

XX 09-AUG-2001.

XX 09-AUG-2001.

```
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver -
XX
XX Claim 1; SEQ ID NO 3467; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX foetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.
XX
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match 20.1%; Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGCCCTCAGATCAAGAAGCCCTCTTGGCTGTGGCCCAACGGTGTGGGGCAGC 60
DB |||||
DB 362 CCTGGCCCTCAGATCAAGAAGCCCTCTTGGCTGTGGCCCAACGGTGTGGGGCAGC 303

QY 61 CCTCTATGGGACAGCAAGACGAGCTTTGTGGGTGAGGAGCGCTGGGGAGTGAAG 120
DB |||||
DB 302 CCTCTATGGGACAGCAAGACGAGCTTTGTGGGTGAGGAGCGCTGGGGAGTGAAG 243

QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTGACGGTGTCTTGGGGCTGATCTCTGATAT 180
DB |||||
DB 242 GGAGATGGAGAGGTGAGGGGAGATCTTGACGGTGTCTTGGGGCTGATCTCTGATAT 183

QY 181 ACCACAAGCTTGGCTTCAGGCCAACGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC 240
DB |||||
DB 182 ACCACAAGCTTGGCTTCAGGCCAACGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC 123

QY 241 GGAGTCTGCATGGCAGCTGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
DB |||||
DB 122 GGAGTCTGCATGGCAGCTGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63

QY 301 ATGACCACTGACACCTTTACCTCCGCTACTGCAATGCCCTGTGC 346
DB |||||
DB 62 ATGACCACTGACACCTTTACCTCCGCTACTGCAATGCCCTGTGC 17

RESULT 4
ABA24907/c
ID ABA24907 standard; DNA; 378 BP.
XX
AC ABA24907;
XX
XX 23-JAN-2002 (first entry)
XX
DE Probe #3373 for gene expression analysis in human heart cell sample.
XX Human; gene expression; heart; microarray; vascular system; probe;
KW
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KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX
XX Claim 1; SEQ ID NO 3373; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
```

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Query Match 20.1%; Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGCCCTCAGATCAAGAAGCCCTCTTGGCTGTGGCCCAACGGTGTGGGGCAGC 60
DB |||||
DB 362 CCTGGCCCTCAGATCAAGAAGCCCTCTTGGCTGTGGCCCAACGGTGTGGGGCAGC 303

QY 61 CCTCTATGGGACAGCAAGACGAGCTTTGTGGGTGAGGAGCGCTGGGGAGTGAAG 120
DB |||||
DB 302 CCTCTATGGGACAGCAAGACGAGCTTTGTGGGTGAGGAGCGCTGGGGAGTGAAG 243

QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTGACGGTGTCTTGGGGCTGATCTCTGATAT 180
DB |||||
DB 242 GGAGATGGAGAGGTGAGGGGAGATCTTGACGGTGTCTTGGGGCTGATCTCTGATAT 183

QY 181 ACCACAAGCTTGGCTTCAGGCCAACGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC 240
DB |||||
DB 182 ACCACAAGCTTGGCTTCAGGCCAACGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC 123

QY 241 GGAGTCTGCATGGCAGCTGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
DB |||||
DB 122 GGAGTCTGCATGGCAGCTGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63

QY 301 ATGACCACTGACACCTTTACCTCCGCTACTGCAATGCCCTGTGC 346
DB |||||
DB 62 ATGACCACTGACACCTTTACCTCCGCTACTGCAATGCCCTGTGC 17
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```
RESULT 5
AAK03423/c
ID AAK03423 standard; DNA; 378 BP.
XX AC AAK03423;
XX XX
DT 05-NOV-2001 (first entry)
XX Human brain expressed single exon probe SEQ ID NO: 3414.
DE Human; brain expressed exon; gene expression analysis; probe;
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX Homo sapiens.
XX WO200157275-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00667.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX Example 4; SEQ ID NO: 3414; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
XX Query Match 20.1%; Score 346; DB 22; Length 378;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-148;
XX Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGCCCTCAGATCAAGAAGGCTTTCTTGCTGTGGTGGCCCAACGGTGTGGGGCAGC 60
DB 362 CCTGGCCCTCAGATCAAGAAGGCTTTCTTGCTGTGGTGGCCCAACGGTGTGGGGCAGC 303
QY 61 CCCTCTATGGGACAGCAAGAAGCAGCTTTTGTGGTGGAGGAGGCTGGGGAGGTGAAG 120
DB 302 CCCTCTATGGGACAGCAAGAAGCAGCTTTTGTGGTGGAGGAGGCTGGGGAGGTGAAG 243
QY 121 GGAGATGGAGGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGCTGATCTCTGATAT 180
DB 242 GGAGATGGAGGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGCTGATCTCTGATAT 183
QY 181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGGAAGTCCATCC 240
DB 182 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGGAAGTCCATCC 123
QY 241 GGAGCTGTCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCTCATCTGTGGAGCCGCT 300
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DB 122 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63
QY 301 ATGACCAGCTGACACCTTTTACCTCCGCTACTGCTGTCATGCCCCCTGTGC 346
DB 62 ATGACCAGCTGACACCTTTTACCTCCGCTACTGCTGTCATGCCCCCTGTGC 17
RESULT 6
AAK28874/c
ID AAK28874 standard; DNA; 378 BP.
XX AC AAK28874;
XX XX
DT 06-NOV-2001 (first entry)
XX Human bone marrow expressed single exon probe SEQ ID NO: 3431.
DE Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX Homo sapiens.
XX WO200157276-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00668.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow -
XX Example 4; SEQ ID NO: 3431; 658pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX the probes of the invention.
XX Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
XX Query Match 20.1%; Score 346; DB 22; Length 378;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-148;
XX Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGCCCTCAGATCAAGAAGGCTTTCTTGCTGTGGTGGCCCAACGGTGTGGGGCAGC 60
DB 362 CCTGGCCCTCAGATCAAGAAGGCTTTCTTGCTGTGGTGGCCCAACGGTGTGGGGCAGC 303
QY 61 CCCTCTATGGGACAGCAAGAAGCAGCTTTTGTGGTGGAGGAGGCTGGGGAGGTGAAG 120
DB 302 CCCTCTATGGGACAGCAAGAAGCAGCTTTTGTGGTGGAGGAGGCTGGGGAGGTGAAG 243
QY 121 GGAGATGGAGGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGCTGATCTCTGATAT 180
DB 242 GGAGATGGAGGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGCTGATCTCTGATAT 183
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OY 181 ACCACAGCTTGGCTTCAGGCCAAGCCAGCCAGGCGCCAGGCTGGAGGAAGTCCATCC 240
Db 182 ACCACAGCTTGGCTTCAGGCCAAGCCAGGCGCCAGGCTGGAGGAAGTCCATCC 123
OY 241 GGAGTCTGCATGGCCAGCTGGAGACCCCTGGGGCTCAATTTCCCCATCTCTGGAGCCGCT 300
Db 122 GGAGTCTGCATGGCCAGCTGGAGACCCCTGGGGCTCAATTTCCCCATCTCTGGAGCCGCT 63
OY 301 ATGACCACTGACACCTTTCACCTCCGCTACTGATGCGCCCTGTGC 346
Db 62 ATGACCACTGACACCTTTCACCTCCGCTACTGATGCGCCCTGTGC 17

RESULT 7
AAI13465/c
ID AAI13465 standard; DNA; 378 BP.
XX
AC AAI13465;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #3398 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN W0200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID No 3398; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match 20.1%; Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTGGCCCTCAGATCAAGAGCCCTTCTTCTGTGGGCCAACGCTGTGGCGGAGC 60
Db 362 CCTGGCCCTCAGATCAAGAGCCCTTCTTGTCTGTGGGCCAACGCTGTGGCGGAGC 303
```

```
OY 61 CCCTCTATGGACAGCAAGAGCAGCTTTGTGGGTGAGGAGAGCTGGGAGGTGAAG 120
Db 302 CCCTCTATGGACAGCAAGAGCAGCTTTGTGGGTGAGGAGAGCTGGGAGGTGAAG 243
OY 121 GGAGATGAGGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 180
Db 242 GGAGATGAGGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 183
OY 181 ACCACAGCTTGGCTTCAGGCCAAGCCAGGCGCCAGGCTGGAGGAAGTCCATCC 240
Db 182 ACCACAGCTTGGCTTCAGGCCAAGCCAGGCGCCAGGCTGGAGGAAGTCCATCC 123
OY 241 GGAGTCTGCATGGCCAGCTGGAGACCCCTGGGGCTCAATTTCCCCATCTCTGGAGCCGCT 300
Db 122 GGAGTCTGCATGGCCAGCTGGAGACCCCTGGGGCTCAATTTCCCCATCTCTGGAGCCGCT 63
OY 301 ATGACCACTGACACCTTTCACCTCCGCTACTGATGCGCCCTGTGC 346
Db 62 ATGACCACTGACACCTTTCACCTCCGCTACTGATGCGCCCTGTGC 17
```

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RESULT 8
AAI134821/c
ID AAI134821 standard; DNA; 378 BP.
XX
AC AAI134821;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #3507 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN W0200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488997/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
PS Claim 25; SEQ ID No 3507; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match 20.1%; Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 CCTGGCCCTCAGATCAAGAGCCCTTCTTGTCTCTGTGGCCCAACGGTGTGCGGCAGC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 362 CTGGCCCTCAGATCAAGAGCCCTTCTTGTCTCTGTGGCCCAACGGTGTGCGGCAGC 303
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 CCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGTGAGGAGGCTGGGAGGTGAAG 120
Db CCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGTGAGGAGGCTGGGAGGTGAAG 243
Qy 121 GGAGATGAGGAGGTGAGGGGAGATCTTTGTACGGTTTCTTGGGGCTGTATCTTGATAT 180
Db GGAGATGAGGAGGTGAGGGGAGATCTTTGTACGGTTTCTTGGGGCTGTATCTTGATAT 183
Qy 181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 240
Db ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 123
Qy 241 GGAGTCTCATGGCCAGCTGGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
Db GGAGTCTCATGGCCAGCTGGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63
Qy 301 ATGACCACTGACACCTTTCACCTCCGCTACTGATGATGCCCTGTGC 346
Db ATGACCACTGACACCTTTCACCTCCGCTACTGATGATGCCCTGTGC 17

RESULT 9
AAI03344/c
ID AAI03344 standard; DNA; 378 BP.
XX AC AAI03344;
XX XX
XX XX
DT 09-OCT-2001 (first entry)
XX DE Probe #3335 used to measure gene expression in human breast sample.
XX XX
XX KW Probe; human; breast disease; proliferative breast disease; non-carcinoma tumour.
XX KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX OS Homo sapiens.
XX XX
XX PN WO200157270-A2.
XX PD 09-AUG-2001.
XX XX
XX 29-JAN-2001; 2001WO-US00661.
XX XX
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
XX XX
XX PT Novel single exon nucleic acid probe used to measuring gene expression
XX PT in a human breast -
XX XX
XX PS Claim 25; SEQ ID No 3335; 322pp; English.
XX XX
XX CC The present invention relates to novel single exon nucleic acid probes.
XX CC The present sequence is one such probe. The probes are useful for
XX CC measuring human gene expression in a human breast sample, where the probe
XX CC hybridises at high stringency to a nucleic acid expressed in the human
XX CC breast. The probes are useful for predicting, diagnosing, grading,
XX CC staging, monitoring and prognosing diseases of the human breast,
XX CC particularly those diseases with polygenic aetiology. The diseases

CC include: breast cancer, disorders of development, inflammatory diseases
CC of the breast, fibrocystic changes, proliferative breast disease and
CC non-carcinoma tumours.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match 20.1%; Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148; Indels 0; Gaps 0;
Matches 346; Conservative 0; Mismatches 0;

Qy 1 CTGTGGCCCTCAGATCAAGAGCCCTTCTTGTCTCTGTGGCCCAACGGTGTGCGGCAGC 60
Db CCTGGCCCTCAGATCAAGAGCCCTTCTTGTCTCTGTGGCCCAACGGTGTGCGGCAGC 303
Qy 61 CCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGTGAGGAGGCTGGGAGGTGAAG 120
Db CCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGTGAGGAGGCTGGGAGGTGAAG 243
Qy 121 GGAGATGAGGAGGTGAGGGGAGATCTTTGTACGGTTTCTTGGGGCTGTATCTTGATAT 180
Db GGAGATGAGGAGGTGAGGGGAGATCTTTGTACGGTTTCTTGGGGCTGTATCTTGATAT 183
Qy 181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 240
Db ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 123
Qy 241 GGAGTCTCATGGCCAGCTGGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
Db GGAGTCTCATGGCCAGCTGGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63
Qy 301 ATGACCACTGACACCTTTCACCTCCGCTACTGATGATGCCCTGTGC 346
Db ATGACCACTGACACCTTTCACCTCCGCTACTGATGATGCCCTGTGC 17

RESULT 10
ABS03407/c
ID ABS03407 standard; DNA; 378 BP.
XX AC ABS03407;
XX XX
DT 19-AUG-2002 (first entry)
XX XX
XX DE Human genome-derived single exon probe from lung SEQ ID No 3398.
XX XX
XX KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
XX KW chronic obstructive pulmonary disease; interstitial lung disease;
XX KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;
XX KW Heremansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX KW pulmonary histiocytosis; lymphangiomyomatosis; Karagener syndrome;
XX KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX KW primary ciliary dyskinesia; pulmonary hypertension;
XX KW hyaline membrane disease.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200186003-A2.
XX XX
XX PD 15-NOV-2001.
XX XX
XX PF 30-JAN-2001; 2001WO-US00665.
XX XX
XX PR 04-FEB-2000; 2000US-180312P.
XX PR 26-MAY-2000; 2000US-207456P.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-234687P.
XX PR 27-SEP-2000; 2000US-236359P.
XX PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX Claim 1; SEQ ID No 3398; 634pp; English.
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12397 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of
CC probes; the novel set of probes which hybridise at high stringency to a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung, comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a single exon
CC probe of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
Query Match 20.1%; Score 346; DB 24; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGCCCTCAGATCAAGAAGCCCTTCTTCTGCTGGGCCAACGGTGTGCGGCAGC 60
DB 362 CCTGGCCCTCAGATCAAGAAGCCCTTCTTCTGCTGGGCCAACGGTGTGCGGCAGC 303
QY 61 CCTCTATGGACAGCAAGACAGAGCTTTTGTGGGTAGGAGAGCGCTGGGAGGTGAAG 120
DB 302 CCTCTATGGACAGCAAGACAGAGCTTTTGTGGGTAGGAGAGCGCTGGGAGGTGAAG 243
QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTGATAT 180
DB 242 GGAGATGGAGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTGATAT 183
QY 181 ACCACAAGCTTGGCTTTCAGGCCAACGCCAGCGGGCCAGGGGTGGAGGAAGTCCATCC 240
|||||

DB 182 ACCACAAGCTTGGCTTTCAGGCCAACGCCAGCGGGCCAGGGTGGAGGAAGTCCATCC 123
QY 241 GGAGTCTGCATGGCCAGCTGGGAGACCTGGGGCTCAATTTCCCATCTCTGGAGCGCT 300
|||||
DB 122 GGAGTCTGCATGGCCAGCTGGGAGACCTGGGGCTCAATTTCCCATCTCTGGAGCGCT 63
QY 301 ATGACCAGCTGACACCTTTTACCTCCGCTACTGCATGCGCCCTGTGC 346
|||||
DB 62 ATGACCAGCTGACACCTTTTACCTCCGCTACTGCATGCGCCCTGTGC 17
RESULT 11
AAH43685
ID AAH43685 standard; cDNA; 1647 BP.
XX
AC AAH43685;
XX
DT 21-JAN-2002 (first entry)
XX
DE PRKAG3 cDNA.
XX
KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
KW metabolic disease; diabetes; obesity; substitution; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 20..1489
FT /tag= a
FT /product= "PRKAG3"
FT variation 230
FT /tag= b
FT /label= "C230G"
FT /note= "Causes P71A"
FT variation 559
FT /tag= c
FT /label= "T559C"
FT /note= "Silent variation"
FT variation 1037
FT /tag= d
FT /label= "C1037T"
FT /note= "Causes R340W"
XX
PN WO200177305-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-SE00765.
XX
PR 07-APR-2000; 2000US-195665P.
XX
PA (AREX-) AREXIS AB.
XX
PI Andersson L, Luthman H, Marklund S;
XX
DR WPI; 2001-657170/75.
DR P-PSDB; Q0847679.
XX
PT New variants of human AMP-activated protein kinase gamma3 subunit
PT associated with a metabolic disease e.g. diabetes or obesity and method
PT for determining a risk estimate of diseases in subject by detecting the
PT variant -
XX
PS Disclosure; Fig 5; 25pp; English.
XX
CC This sequence represents the full length cDNA encoding the human
CC AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting
CC the presence of the PRKAG3 DNA, or a variant, is useful in determining
CC a risk estimate of a metabolic disease, such as diabetes or obesity,
CC in a subject. The variation may occur in exons 3, 4 or 10. In exon
CC 3 variation may be a substitution of a G for a C at nucleotide 320,
CC resulting in the amino acid substitution P71A; in exon 4 variation may
CC be a substitution of a T for a C at nucleotide 550; and in exon 10

CC variation may be a substitution of a T for a C at nucleotide 1037,
CC resulting in the amino acid substitution R340W. There may also be
CC nucleotide variation in intron 6. The numbering of these
CC variations is based on the full length cDNA as given, rather than on
CC position 1 of the open reading frame.
XX
SQ

Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;

Query Match 9.8%; Score 168; DB 22; Length 1647;
Best Local Similarity 100.0%; Pred. No. 6e-67;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1523 GGTTCCTGCTGCCCCGCGCCCTCTCTACCGCACTATCCAAAGATTGGGCATCGGC 1582
|||||

Db 1022 GTTTCCTGCTGCCCCGCGCCCTCTCTACCGCACTATCCAAAGATTGGGCATCGGC 1081
|||||

Qy 1583 ACATTCCGAGACTTGGCTGTGGTCTGGAGACAGACCCATCTGACTGCGACTGGACATC 1642
|||||

Db 1082 ACATTCCGAGACTTGGCTGTGGTCTGGAGACAGACCCATCTGACTGCGACTGGACATC 1141
|||||

Qy 1643 TTTGTGGACCGCGCTGTGCTGCACTCCCTGTGTCACCAATGTGGT 1690
|||||

Db 1142 TTTGTGGACCGCGCTGTGCTGCACTCCCTGTGTCACCAATGTGGT 1189
|||||

RESULT 12

AAD03296
ID AAD03296 standard; DNA; 2109 BP.

XX AC AAD03296;

XX DT 13-JUN-2001 (first entry)

XX DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.

XX KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.
XX OS Homo sapiens.

XX FH Key

XX FT 5'UTR Location/Qualifiers
1..471
/*tag= a

XX FT CDS 472..1389
/*tag= b

XX FT FT 1390..2109
/*tag= c

XX FT 3'UTR "Human Prkag3 protein"

XX FT WO200120003-A2.

XX PD 22-MAR-2001.

XX PF 11-SEP-2000; 2000WO-EP09896.

XX PR 10-SEP-1999; 99EP-0402236.

XX PR 18-MAY-2000; 2000EP-0401388.

XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX PA (ANDE/) ANDERSON L.

XX PA (LOOF/) LOOFT C.

XX PA (KALM/) KALM E.

XX PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;

XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;

XX DR WPI: 2001-244810/25.

XX DR P-PSDB; AAE00221.

XX PT New variants of the gamma subunit of vertebrate adenosine

XX PF monophosphate-activated kinase for diagnosis or treatment of disorders

PT associated with energy metabolism such as diabetes, obesity, and
PT myopathy

XX Claim 12; Fig 2; 71pp; English.

CC The present sequence is a cDNA encoding human adenosine monophosphate
CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
CC PRKAG3. Mutation in Prkag3 results in an altered regulation of
CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
CC useful as therapeutic for treating carbohydrate metabolism disorders such
CC as diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.

XX SQ Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;

Query Match 9.8%; Score 168; DB 22; Length 2109;
Best Local Similarity 100.0%; Pred. No. 5.9e-67;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1523 GGTTCCTGCTGCCCCGCGCCCTCTCTACCGCACTATCCAAAGATTGGGCATCGGC 1582
|||||

Db 922 GTTTCCTGCTGCCCCGCGCCCTCTCTCTACCGCACTATCCAAAGATTGGGCATCGGC 981
|||||

Qy 1583 ACATTCCGAGACTTGGCTGTGGTCTGGAGACAGACCCATCTGACTGCGACTGGACATC 1642
|||||

Db 982 ACATTCCGAGACTTGGCTGTGGTCTGGAGACAGACCCATCTGACTGCGACTGGACATC 1041
|||||

Qy 1643 TTTGTGGACCGCGCTGTGCTGCACTCCCTGTGTCACCAATGTGGT 1690
|||||

Db 1042 TTTGTGGACCGCGCTGTGCTGCACTCCCTGTGTCACCAATGTGGT 1089
|||||

RESULT 13

AAD03320

ID AAD03320 standard; cDNA; 2115 BP.

XX AC AAD03320;

XX DT 13-JUN-2001 (first entry)

XX DE Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.

XX KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.
XX OS Homo sapiens.

XX FH Key

XX FT CDS Location/Qualifiers
1..1395
/*tag= a

XX FT FT /product= "Human complete Prkag3 protein"

XX PN WO200120003-A2.

XX PD 22-MAR-2001.

XX PF 11-SEP-2000; 2000WO-EP09896.

XX XX


```
XX SQ Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;
Query Match      8.5%; Score 147; DB 22; Length 547;
Best Local Similarity 100.0%; Pred. No. 2.8e-57;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1523 GGTTCCTCGTCCCGCCGCTCTCTCTACCGCACTATCCAAGATTGGGCATCGGC 1582
Db      |||||||
QY 1583 ACATTCCGAGACTTGGCTGTGGTGTGGAGACAGCAGCACCACCTCTGACTGCACATCGACATC 1642
Db      |||||||
QY 1643 TTTGTGGACCGCGGTGTCTGCACTG 1669
Db      |||||||
QY 405 TTTGTGGACCGCGGTGTCTGCACTG 431

RESULT 15
ABA49850/c
ID ABA49850 standard; DNA; 92 BP.
XX AC ABA49850;
XX DT 01-FEB-2002 (first entry)
XX DE Human breast cell single exon nucleic acid probe #8545.
XX KW Human; microarray; single exon probe; gene expression; breast;
XX KW disease; cancer; ss.
XX OS Homo sapiens.
XX PN WO200157271-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000662.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.
XX PT New spatially-addressable set of single exon nucleic acid probes,
XX PT useful for measuring gene expression in sample derived from human
XX PT breast, comprises number of single exon nucleic acid probes -
XX PS Claim 4; SEQ ID NO 8545; 327pp + sequence listing; English.
XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human breast and BT 474 cells. The method involves contacting
XX CC the probes with a collection of detectably labelled nucleic acids
XX CC derived from mRNA of human breast, and then measuring the label
XX CC bound to each probe of the microarray. The probes are useful for
XX CC verifying the expression of regions of genomic DNA predicted to
XX CC encode proteins. They are useful for gene discovery, and for
XX CC determining predisposition and/or prognosing breast disease. Gene
XX CC expression analysis is useful for assessing the toxicity of chemical
XX CC agents on cells. The microarray of this invention presents a far greater
XX CC diversity of probes for measuring gene expression, with far less bias
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CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 92 BP; 22 A; 24 C; 34 G; 12 T; 0 other;
Query Match      3.8%; Score 65; DB 22; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGCCCTCAGATCAAGAGCCCTTCTTTGCTCTGGTGCCCAACGGTGTGCGGGCAGC 60
Db      |||||||
QY 61 CCCTC 65
Db      |||||
Db      5 CCCTC 1

Search completed: January 6, 2003, 09:55:47
Job time : 336.168 secs
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